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<b>(21) International Application Number:</b> PCT/US97/20313 <b>(22) International Filing Date:</b> 5 November 1997 (05.11.97)  <b>(30) Priority Data:</b> 60/030,455                      6 November 1996 (06.11.96)                      US  <b>(71) Applicant (for all designated States except US):</b> WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Mass- achusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA).  <b>(74) Agents:</b> GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).		<b>(81) Designated States:</b> JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
<b>(54) Title:</b> BIALLELIC MARKERS  <b>(57) Abstract</b>  The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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-1-

## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996,  
5 the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution,  
10 generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and  
15 is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In  
20 many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism  
25 (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

-2-

RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater



-3-

frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays

10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for

15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to

20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

-4-

## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

-5-

## DETAILED DESCRIPTION OF THE INVENTION

## DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

-6-

polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with

15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same

20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site

25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include

30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

-7-

and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

-8-

conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

-9-

and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

-10-

samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For  
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),  
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification  
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

#### 30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,



-11-

sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 20 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

-12-

hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

-13-

sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of  
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of  
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30 1988)).

-14-

## 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

## 10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

## 25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

-15-

## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

-16-

match of suspect and crime scene sample would occur by chance.

- $p(\text{ID})$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):
- 10 Homozygote:  $p(\text{AA}) = x^2$
  - Homozygote:  $p(\text{BB}) = y^2 = (1-x)^2$
  - Single Heterozygote:  $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$
  - Both Heterozygotes:  $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

- The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:
- 15  $p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2$ .

- These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(\text{ID})$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:
- 20  $p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(\text{ID})$  and  $p(\text{exc})$ .

- The cumulative probability of identity ( $\text{cum } p(\text{ID})$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.
- 30  $\text{cum } p(\text{ID}) = p(\text{ID1})p(\text{ID2})p(\text{ID3})\dots p(\text{IDn})$

-17-

The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5        If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10        B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15        Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20        If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child  
25        attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30        The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

-18-

incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the



-19-

circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

-20-

(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\chi^2$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner

-21-

might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year-season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

-22-

D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a  
5 Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next  
10 generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present  
15 section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such  
20 analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84,  
25 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6  
30 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

-23-

for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ), ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$  to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

-24-

Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component) except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

-25-

corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

-26-

The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, 5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is 10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene 15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating 20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate



-27-

the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and  
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to  
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide-fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*  
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of  
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific  
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

-28-

100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

#### 15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

-29-

comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

-30-

corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

-31-

All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACCTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACACATGCCAGTTGGGAAGTCT GAAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAGAGAGAGTGGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATTTGGAAAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTGCTTTTC/TAGTTTAAATGCTGTCTCTGTCCAG
WI-7070	226	C	T	---	---	AAGCCATTGACGTAACTCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAAGGAC/GC/JAA AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTT GATAATACATAAAGCCCCCTAGGATTTAGATACAATCTTGAAGAACTGAGACAGATAATCTGAATT AAATGAGGTAAAGTTTCAGGCACTCA
WI-10744	61	G	C	---	---	GGGCAAAATTACCAGCAAAAAGTCAAAATACCAGCATCAAAGTCAGGTGCAAAAGAGGTAGAACAA TTACAGTAACATATGTCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCTAGAAATG/C/TJAGTG GGTCCCTAAATAGTTATTAGTCCCTTTTCTCTCTCTCTCACTCTGAAATTTTATATACTTAA GGGATTAGTTACCACCAAAATGTGTATGATCAATTTGATTCCTACTGAA
WI-9975	126	C	T	---	---	GCTAGGTTTGTCTCTGTTGGCTGCTTCACTAGACTTGAGATGACTTGATTACAGTAATCCCTATGT GATGTAACATAGCTAGACCTTCCCTTCTCCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC TCAACCTTCTCTCCAGTTCATCTGATTAATTTCTTCCCATATTAATTCAAAGGAGTGGACAGGT CCCTGGCTGAAAAGAAATAAAGAGATCCCAAGTGGTGGGG/G/TJCTT
WI-8010	247	G	T	---	---	GCCGGGCTATCTTTTAATTTAACTTGTATCTTTGGTGTTTCTCCATCTCCTAGGATTCTGCCTTATAAT CTTTGTCTGTCTGTA/GC/JATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTCCCAATCTTCAGGTCTCTTGAATTTTCTCTGCTATTGAGGACATTCACACTTCTACTTAA TCTCGACTCTATAACAACCTCCAAACAGAA
WI-5222b	85	G	C	---	---	GCCGGGCTATCTTTTAATTTAACTTGTATCTTTGGTGTTTCTCCATCTG/C/JGATTCTGCCTTAT AATCTTTGTCTGTCTGTAGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTCCCAATCTTCAGGTCTCTTGAATTTTCTCTGCTATTGAGGACATTCACACTTCTACTTAA TCTCGACTCTATAACAACCTCCAAACAGAA
WI-5222	52	G	C	---	---	TATGCATTCACAAAAGCGATATAATTTAAAAGTTTTTTTCAATTAGAAATAAATGTATAAAAATAA ATATGTTATTATAGGCATTTTACTAACTATAGTCTCTTGGGAAGGAACACCCAAACCAATACTT ATAAAGTACATGTAATTTATAGTAACATAATTTACTATATACATATGGAATAATCATATTTCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGGAC/GC/JAAGCTGCTG
WI-8007	242	C	A	---	---	TCAGTTGCAAAAATGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGATGTGTTTTGTTAG TCTATATTCACACATATGAGTGAAATTTTC/TJGGGCGCATGGGAAATACATCTTTATGAGACATGGA ACTGCTCACCACATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATTCCTTTGTTTAC ATGCTTTCCAATCTGATTTTGTATGACTATTGTATGCACAGTTGGATCACC
WI-9823	97	C	T	---	---	

WI-9551b	105 A T ---	---	TCTACATCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTTCCCT ACTTGCTCCTCATGTACAAATTTTCTGCTGCTCTTCA/ATGGGGCAGCTTGAAGCCCTCCCTTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCTCTG CTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTGAATGTCCTC
WI-9651	139 T C ---	---	TCTACATCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTTCCCT ACTTGCTCCTCATGTACAAATTTTCTGCTGCTCTTCAAGGGGCAGCTTGAAGCCCTCCTTTAGACACCT CT/CACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCTCTGT CTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTGAATGTCCTC
WI-7676b	309 A C ---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGCTGGGACCTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCGGCTCTCTTGGTGCCTGCTGGTTCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGGTGC TCCCCCGCTCCTCGAGGCGAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGCTGGGACCTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGTAGATGGGAGGGTCTGTGTGAAGGG GC/ATGGCTCTCTTGGTGCCTGCTGGTTCAGGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGCTCCTCGAGGCGAGTATAGGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTTGCTTGGGCTGTTCATTCACTTTCCTCTCTCCAATGAAGAGGATATTTAAGCATCAAT CATCTGGCCCTTTTGTAGTTTGAATAATTTTGTG/ATGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAGGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAATAATCTTT
WI-9986	42 T C ---	---	TTGGTGTGAACCTCAGAAATAGGGAAAATAGACAATTTGAAT/A,CJGTACCCAGGAAACAGAG CCCTGCACTTGACTCCAAAGGAGTTCTATATCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTACAAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAAT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATCAGGCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCTCAGAGAGCTGAAAGGGTCCCTCGGCTTTTATTT CAGGGCTTTCATGCGCTCTATTCCCCCTCTGCTCTC/CAGCACTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAAACAAGCTCAITTTGTACAGTGTCTTTCATGTAAATA
WI-7224	134 T C ---	---	ATAAACCTTGTGTATGTATCACCACCACTCAATAATTCAACTTATGTGCTATCAGATATCCTCTCT ACCCCTCAGGTTATTTGAAGAAAATCCTTAACATCAAAATCTTTCATCCATAAAATGTGAGCATTT /CJATTAANAACAATAAATCTTTTAAAGAAAACATAAGGACACATTTTCAATTAATAAAATAAAG GCATTTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132 A C ---	---	---	TCTATTGCAATTCACAGTAGCCCCATGAAGTAGGTAGGTATACCAGCCTCTATTTTAAATGAGAAGAT GGAGGCCCTTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCTTAATAAGCAAAGACCTGCA[AVC JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTTGCTGTCAGCCAGGACCCCATGGCA GAAAGCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145 G A ---	---	---	AGATCTGCCATTAGTATTTATCTTTGAAGATACITTTGGAGATTCAITTTCTTGAGTGGCACTGCAAT GCTCATTGAGTGAACACITTTGGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACTGCTCCTTAGGCATTGAAACCATCACCTGGTTTGCAITCTTG ATGACTGAGGTTTAACTTAAATGACIGAGGTTAACTTAAAC
WI-1021	24 A T ---	---	---	AAACACACAGAAATCATCAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAAGTAACTCTGAAATAGTAGGATAGTATTATCATTTCTGTATAGATTCACTCTCAGCAAT TGGTCTGTTTTCATTTCTATGGAACCTCTCCGTAAGTAAATTTTCAITCTATGGAACCTCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAGAACACITTTGAATGGTCTTGTC TTTCAATAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCCTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGATTAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAACCAAGAGAAAGAACTTGAT
WI-4719b	107 T G ---	---	---	TTCAITTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGCTTTGGGTGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCAATAGTGACTTGAGAGTTTACAGTTTACAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAATCAC TGCTCAAAATCCCCACTTGTCACCTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	---	TTCAITTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGCTTTGGGTGTGAGCGGATT AT[G/A]CTGACGCCATGGGTGTTTCAATAGTGACTTGAGAGTTTACAGTTTACAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAATCAC TGCTCAAAATCCCCACTTGTCACCTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	---	TCAACACGCTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTTACCCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTACCACCTTCTCTCTGACACTGCCAAGT TAAAGAAACCCCTGCTTCTGCTGGAGAGGGAGGGCCAGACAGGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACCCAGGGTTCCAACTTT
WI-9484	178 G A ---	---	---	TCAACACGCTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTTACCCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGGTGTACCACCTTCTCTCTGACACTGCCAAGT TAAAGAAACCCCTGCTTCTGCTGGAGAGGGAGGGCCAGACAGG[G/A]AGGAAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCCAGGGTTCCAACTTT



WI-7330	207	C T	---	---	AGGATGGAAGGAGACACGGGGCAGGGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAATTTGGGCATATAGGTTT GTGACACAAGAAAGTCATACTTTGGTGGCTAAGTTTCTAAAGGAAATAACTGAAAGATTTAAAG TGAGAG[C/T]TGAAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGCACAG
WI-9443	211	G A	---	---	TTAAAAACAGTTTCAGGTTGGTGAAGCAGAAAGGGATGTATTACAAATTTAAATGAATCAGTCACCT GCACAATTAATCTCTTGGCATACATAAACTGGGTTTAAATGGCAATGATGACATCATAGCATGA CCAACACTCATGGAAGGCAGTCTAGAGTCCATCACGCTACACCTGAGGGGAAGGCACACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCATGCCACTT
WI-7166	59	C T	---	---	TCTCTCAAAAGAGAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTCCTTGTGCAAAATATTTGACTATCTGTATCTTTCATCCTTGACTAAATTCGTG ATTTCAAGCAGCATCTCTGTTTAACTGTTTGTGTGAACAAATGTGAAAGAGTCTTCCAAT TAATGCTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCGAG
WI-7259b	189	T C	---	---	GCTCTTCCCCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGAGCGGGAGCAATTTAGCC CCACCCTGCTCCCATCTGCCCTGCAACAGCTGCAAGCTGCTTCTCTCTGAGTTCTCTGGCT GGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[T/C]TGGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGCTC
WI-7259	188	G T	---	---	GCTCTTCCCCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGAGCGGGAGCAATTTAGCC CCACCCTGCTCCCATCTGCCCTGCAACAGCTGCAAGCTGCTTCTCTCTGAGTTCTCTGGCT GGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[G/C]TJTTGGGGAGCA GAGCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCTGGAGC
WI-7322	275	A G	---	---	GTACTTTAGGCTGTGGAGGTGGCATTTAGTGGTGACCTTGACCCAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAACTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATAG GCCATAAAGTGCCTAAGCACTCAGGCTCCCACTCCCACTCATCAACCCCTTGACCAGAGAAAGCACTC TGGTTCTCTATCCCTTGTACATAGAGATTGTGCATGGGGCTCTGGCTG
WI-7685	46	T C	---	---	TCAGTTCTAGTCTCTCTGGGGCCACACAGAACTCTTTTGGGCTG[T/C]TTTCTCCCTCTGGATCA AAGTAGGCAGGACCATGGGACCAGGTCTTGGAGCTGAGCTGAGCTCTACCTGTACTCTTCGAAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTGTATCTCCATGGCTTCTCTCCCTCTGCGGACTC CTGGGTTGAGCTGTTGCCTCAGTCCCCCAACAGATGCTTTCTGCTC
WI-563	87	G A	---	---	TGTGACCAATTTGTTATTTTAGAGGGTTTAAACAATGGCTGACTATACCTGATGGTCGCCAGAAATTC CTGGGGGAGGGCTCCCT[G/A]CCTGTATCATGTCTACCTAACCTGCTACTCTAACAACTACTCC TGTGGTATGGGATCCTAAGCCAAAAAGCTGAATGAACATGTTCTAGCACTACAGAAATCCACT GCCCTCAGTAAGGCCAAATTTTAAATCTCTTTGGATAACCCAGGGCACAT

WI-931c	191 C A ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCTTCT GTTGCTGCACCTGTCTATTACTGTTGTATGGATTATATTATGTCCTCAAAAAGCC[C]A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCCTCCCTA]G]TCCCCTCACCACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTATTACTGTTGTATGGATTATATAATTATGTCAAAAAGCCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAAGCCAC]A]G]GCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTTCTCTCCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATTCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTATTACTGTTGTATGGATTATATAATTATGTCAAAAAGCCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91 C T ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACAACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGG[C]T]ACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCCOC TTAGCAGCAGAAATACAAGAAATCTTGGACCTGTACTCTGATACAAAATAAGGACATGGGTACGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCC
WI-10870	103 G A ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACAACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGACACCTACTTAGA]G]A]G]AGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATACAAGAAATCTTGGACCTGTACTCTGATACAAAATAAGGACATGGGTACGC CTGAGCCACTCTTAAACCATGAACCATCACCATTTAAATAACGTTGCCCCC
WI-7719b	281 T C ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTTGGCTGGCCAGTCTACAAATGTCCCAATATCAAGGACAAACCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTTGCCCATGTATAATCCTCAGTATGATTTCAAGCTAAAGCAA
WI-7719	163 A G ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTTGGCTGGCCAGTCTACAAATGTCCCAATATCAAGGACAAACCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC]A]G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTTGCCCATGTATAATCCTCAGTATGATTTCAAGCTAAA
WI-10396	72 C A ---	---	GCCTGGAGTATATCTAACTGTGGCCCTCCACTTTCTTCTTGAACATTTGCTATCAACTGGGAA GAGT[C]A]TGTGACTTTATGCCAGTTTCCCCTCTCAGATTTTATGACGGTTGTTTCTTTTGTGA TGCCATTTGAGGGATTGATGTTTCTTAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTTTCAGG TTAACAGCCACCATTTGTAACACTTTGT

WI-10673	94 C G ---	---	TCCCTTTATGCACCCCAAGAGATATTTAAACACCAATACGTAGCAGGCCATGGCTCATGGGAOC CACCCCGTGGCACTCATGGAGGGGCG/GTGCAGGTGGAACATATGCAGTGTCTCCGGCCACACA TCCTGTGGCCCCCTACCTGCCCAATTCATCTGCAATTAATCTGCTTATTTGTTTCATCCTG GAGAAITGAAGGGGAGGTCAGTTGTTGTCATGATTGTCAGAGAACCCT
WI-7842	57 T C ---	---	CACAGCCATGCCCTTGAGAGCGGCCACAGATGCTGAATCCCTATCCCCATCTGT/CJGTATGAG TCCCAITTTGCCCTTGCAATTAGCATTTCTCTCCCCAAAAAGAAATGTGCTATGAAGCTTTCTTTCCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGTAGTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---	---	CTGCCTCATCAGCCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGACAAAGGGGGCCACATCCCCACCCAGCTGTACCCAGCCGGGCAGGTGCAGCCCTTCCTCCC TGCTCTGCJ/CJCTGACTCTCTTTGAGGTCCCTGTATGTCTACCTCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCCATTCCTCTTACTGGGSCCTGGGGCTCTAGCCCAA
WI-4767b	173 C A ---	---	TTCCAGTCTGTTTATCCTTTTATCCTTTGTCAAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCCT CAGGTCTGGGTAATCCTAGATCTTCCCTATATCCATTGAGTGTGAGTGGAGAGAGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACA/CJAATCACTAAGGAAATCCACTAAGA CTCCTCTAACCCAGAGATTTTAAACCT
WI-4767	50 A G ---	---	TTCCAGTCTGTTTATCCTTTTATCCTTTGTCAAAAAGATGCTCTTAGACTGAJVGJATTCATAAAGAGTT CCTCAGGTCTGGTAACTCCTAGATCTTCCCTATATCCATTGAGTGTGAGTGGAGAGAGGGTATG TTCTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAAATCCACTAAGAC TCCTCTAACCCAGAGATTTTAAACCT
WI-7718f	222 C T ---	---	ATTGCACCTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAAGTTCACTACATGTTCTGGGGCCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAAAGCTGTGTTGAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAAJ/CJTCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718e	60 T C ---	---	ATTGCACCTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAJ/CJGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAAGTTCACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTCAGATGGAAGAGGTGAAATGAAGAGGAAAGCTGTGTTGAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT
WI-7718d	31 G A ---	---	ATTGCACCTGAAGTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAAGTTCACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTCAGATGGAAGAGGTGAAATGAAGAGGAAAGCTGTGTTGAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAAT

WI-7718c	248	A G ---	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAACACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248	A G ---	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAACACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAGAACCATGCAGGAAGGAAAACTATGTATT[AG/G]AT
WI-7718a	42	A T ---	---	---	ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGC[A/C]TGTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAACACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAGAACCATGCAGGAAGGAAAACTATGTATTA
WI-7227d	99	G C ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGTGTAAAGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCACCCAGCGACTAATG
WI-7227c	291	G A ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTTAGTATCTGTGTTCCGGTGGTGTAAAGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACAGTG TTATTATGGGAAAGGAAATGGCATTGCTGCTTTCACCCAGCGACTAATGCAAT
WI-7227b	93	G T ---	---	---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGTGTAAAGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCACCCAGCGACTAATG
WI-7227a	24	A G ---	---	---	AGGGAATTGTGTTGCTCCTGGAGG[AG/G]AGCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGC TTCCGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGTGTAAAGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCACCCAGCGACTAATG
WI-7310b	234	A C ---	---	---	CCACAATGCCTCTCCACGATGTCAGGACTCCTGCTGCTCTGGAGGAGACAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGCTACTGCTATGTTGATGCTTTCATCGAACAACTGATGCGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACAGGCAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[AC/G]ATGATCTTGAGATTTC

WI-7310a	64 T A ---			CCACAATGCCTCTCCACGATGTCAAGGACTCCTGCTGCTGCTGAGGTGGGAGACAAGGAACQTTA JCGAAGAGGAGCAAGCAAGCCGCTACTGTCTATGTTGTGATCCTTCATCGAACAACTGATCGGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGACATGTCTATTGAACAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---			CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCCTGCTGGTTGATAATAATCA GATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAATCGTCC CTGAGGAGAAATCTGGGAGGAGCTGAGTGATGAAGGTGATGTTGGGAGGGAGCACAGTGT CTGTGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAAACTA
WI-7878a	51 C G ---			CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCCTGCTGGTTGATAATAA TCAGATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAATGC GTCCCTGAGGAGAAAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGATGTTGGGAGGGAGCACAGTG TCTGTGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAAACTA
WI-7381c	213 C T ---			CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTCTACC AGCCCTGCAAGTTTCTCATGAGCGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAGATC AGATGTGCCAAGGGAAGGAGCTGCTGGTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAGACA AAACGGCCTCCTGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---			CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTGCTTCTTCTCT ACGAGCCCTGCAAGTTTCTCATGAGCGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGGAAGGAGCTGCTGGTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---			CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTGCTTCTTCTCT ACGAGCCCTGCAAGTTTCTCATGAGCGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGGAAGGAGCTGCTGGTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---			AAATTGCTCTATTGGACCCCTCATATTAATAAGAGCAATGAGAGCGGGAATTTGAATCTCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GATGTAGATTGTACATTCATCTGAAACAAACCTTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGAGGTTTTGTCCC
WI-1017a	92 G A ---			AAATTGCTCTATTGGACCCCTCATATTAATAAGAGCAATGAGAGCGGGAATTTGAATCTCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GGATGTAGATTGTACATTCATCTGAAACAAACCTTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGAGGTTTTGTCCC

WI-1795b	130	T C ---	---	GAAGCAACCCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTTCTCCAGACTCTCAGGATTA AATTGTATGCATGTGAACAACCTGAGGTACTTTAGATCTCAGTGCCTTGCGAGAAAGAAAGTTC/C GTCTACCACTTTTCAACCAAAATTCGTAGTACAATTTAAGTATCTCTTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47	T C ---	---	GAAGCAACCCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTTTCCTCCAGACTCTCAGG TTAAATTGTATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTGCCTTGCGAGAAAGAAAGTC GTCTACCACTTTTCAACCAAAATTCGTAGTACAATTTAAGTATCTCTTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136	G A ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCCATACGTAGGTCTTGGTCTCTCTATCACAATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCGCAGTCCCTCTGAGACTCCC ATGGATCATCTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616c	136	G A ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCCATACGTAGGTCTTGGTCTCTCTATCACAATTGCCA C/GAJTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCGCAGTCCCTCTGAGACTCCC ATGGATCATCTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616b	141	C T ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCCATACGTAGGTCTTGGTCTCTCTATCACAATTGCCA CGTAGC/CJCTCCCTTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCGCAGTCCCTCTGAGACTCCC ATGGATCATCTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616a	116	G C ---	---	CACACAATTTGCAAAACACTTCAAAGTGAACGCCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTTGGTCTCTCTATCACAATTG CCAGTAGCCCTCCCTTCCCTTCCCTTCCCTACAGGCCCTCTTACAGGCCCGCAGTCCCTCTGAGACTCCC ATGGATCATCTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-1126c	52	G A ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTTCCAGTATCAGTATCACTG/AJATACTAATAA AAACCCCTGTAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCCGCAAGAAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATAATTTAATTTCAAGTTTCCCTCAAAAGGAATATGAAATT TGTTAAAAATGCAAAATCCAGCTGAACCTTTTTTGGACTGTGCTTTTATTTCTTT
WI-1126b	230	T C ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTTCCAGTATCAGTATCACTAATAATAAAA CCCTGTAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCCGCAAGAAAGAAAT TTATTTCTCAAGATATAAAAAATAAATAATTTAATTTCAAGTTTCCCTCAAAAGGAATATGAAATTTGTT AAATGCAAAATCCAGCTGAACCTTTTTT/CJGGACTGTGCTTTTATTTCTTT

WI-1126a	97	T C	---			CTCTATTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCAGTACTGATACTAATAATAAAAA CCCTGTAAGTCTGCTTTGCATTTTCAAGATTTC/CAATATATATCCAGATTGTTTCCAGCAAGAAA ATTTTATTCTCAAGATATAAAAAATAAATAATTTAAATTCAGTTTCTCAAAAGGAATATGAAATTT GTTAAATGCAAAATCCAGCTGTAACTTTTGGACTTGCTTTTATTTCTT
WI-11183c	124	C T	---			TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACTAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192	T C	---			TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACTAACATTT ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATTC/CAATTTGGT ATGGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118	C T	---			TAGTGCTAATTTTGGAAAAGTTTGGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGC/CTTGTGCTACATAACA TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTAAATATTGGT ATGGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174	G A	---			GCTTGGTTTGGCTTTAGTCTTATTGTCTCAGTCTTGAGTCTCCCTTCTGCTGGCCCTTTTGATTTCA CCCATACCTCTATGCCCTGCTCAGACCAATTTCCCTATCTGAGCGCTCTTCTTGTACTTTCTCTG TTCACCAACCTTCTTTTATTCTTCAGGACACTCA/GA/JTTCACATGCCACTCTCGTGACACTGCTCT TTCACATCTTCTGTGTCCTTTTCCC
WI-10770a	49	G T	---			GCTTGGTTTGGCTTTAGTCTTATTGTCTCAGTCTTGAGTCTCCCTTCTG/TTGCTGGCCCTTTTGATTT TCACCCATACCTCTATGCCCTGCTCAGACCAATTTCCCTATCTGAGCGCTCTTCTTGTACTTTCTC CTGTTCAACCAACCTTCTTTTATTCTTCAGGACACTCAGTTCACATGCCACTCTCGTGACACTGCTCT TTCACATCTTCTGTGTCCTTTTCCC
WI-9667b	82	C T	---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCAGTCTTGAGTCTCCCTTCTCAATCTGCTGATCATGG TTATCACTGGACA/C/JAGCCACCTCCCAGCAGGCTTAGAACCTCATGAGTAAGGACCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCAATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCAATCT
WI-9667a	68	G C	---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCAGTCTTGAGTCTCCCTTCTCAATCTGCTGATCATG G/CJTATCACTGGACACAGCCACCTCCCAGCAGGCTTAGAACCTCATGAGTAAGGACCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCAATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAAACTTGCAATCT

WI-10400d	189 A G ---			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTATTCTAAATTT TCITTCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTC[A/G]TGCCATGTAG TTTTTGGTTCAITTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTATTCTAAATTT TCITTCCTTACCTTTACTCTCCCAACCA[A/C]AAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCAITTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTATTCTAAATTT TCITTCCTTACCTTTACTCTCCCAACCC[A/G]AAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCAITTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAAT[C/T]GCAATTCAGACATCT GCTGGTTAACTGTTAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTATTCTA ATTTTCTTTCCCTTACCTTTACTCTCCCAACCAAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCAITTTACTTGCAAATATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---			AAAGGGCTACAACTAAGGCCAAACCAATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTACCA[C/T]TAGAAAGGGCAATTTCAAGCACATTCATGAGGCTTCATATACTGTTAG CAACAAATGGAATGTATTAGCCCAAGGCGAGGTATGGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---			AAAGGGCTACAACTAAGGCCAAACCAATGAAC[C/T]GGTATAAGGAGGGTAAATGCAAGGGGAGA CCCACTCTACCACTTAGAAAGGGCAATTTCAAGCACATTCATGAGGCTTCATATACTGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCGAGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATAGTGTAGATGCTGGGCTGTCTCTCCCTTCCAGGAATGCTGGGCCCCCAGCTGGCCAGAC AAGAAGACTGTCAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAATAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATAGTGTAGATGCTGGGCTGTCTCTCCCTTCCAGGAATGCTGGGCCCCCAGCTGGCCAGAC AAGA[A/C]GACTGTCAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCATTTATGGTGTAGTTCTGA



WI-7038a	31	G A	---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGG[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTTG TCCCAATGAATACTGAGATGCTGGGCTGCTCTCCCTCCAGGAATGCTGGCCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGTCGGAGTCTGTAACCAAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCTATTTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	---	ATACGCTTCTGTCTGTCCACAGTGAACCAAGCAGCACCAGGTGGCCAGGGTCGGGCTCCACACA[G/T] CCCTCAGCCCCCTCAGCTTTCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATCCCAAGTCTCCTCCTCGGATTTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGCTTCTGTCTGTCCACAGTGAACCAAGCAGCACCAGGTGGCCAGGGTCGGGCTCCACAC[CT/AG] CCCTCAGCCCCCTCAGCTTTCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATCCCAAGTCTCCTCCTCGGATTTGGATCTAGCAAGACCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATTCCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTAGCCCCCATCTCT[G/A]TGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTCT TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGAT[TA/TA]AAGAGTGAGTGACGGTGA CCTGTAGCCCCCATCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTCT TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAA[TA/TA]AAGAGTGAGTGACGGTGA CCTGTAGCCCCCATCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTCT TTTTGGCAGGGGACACTCTCTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6711b	226	G T	---	---	GGCTATTTGTAAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAACTTCACTTCCAATCACTGAAT TTCATATACCTCCATTATTAATCAATACATCATTCAGAGAGAAAGACACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGTATCTCTAAA
WI-6711a	361	T C	---	---	GGCTATTTGTAAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAACTTCACTTCCAATCACTCT GAATTCATATACCTCCATTATTAATCAATACATCATTCAGAGAGAAAGACACGGTGCCAACTG GGTTGGTTGGTGCCTGCACACCCACAGTGGCAACTAAGTGTATCTCTAAA

WI-10613b	172	A C ---	---	ATGTATGCCAAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTGAGCCATA TGGTGAATAATTTAGAAAGTATTATCTCTATATGTATATCTAGCTTTAACATCAATGAATGTGATTT TTTGTCACACTTTTGACAAGGCCAGGCAATTTTATTTG[A/C]GCCCTAGGAGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-10613a	44	G A ---	---	ATTGTATGCCAAAATCATAATACCCCTGCATTCTAGAAACATACA[G/A]GTAAATAGAAATTTGAGCC ATATGGTGAATAATTTAGAAAGTATTATCTCTATATGTATATCTAGCTTTAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-7587c	133	A T ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA[A/ T]GGAATGAACCACTCCCTGCCATTCCCTATAAGATATCCCAAGACCCAGGCAATTTGCCCTCT TTCCACATGCCCTCCCATATGCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587b	81	G A ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGATATCCCAAGACCCAGGCAATTTGCCCTCT TCCACATGCCCTCCCATATGCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587a	28	C T ---	---	GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCCTTGA AGCACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGATATCCCAAGACCCAGGCAATTTGCCCTCT TCCACATGCCCTCCCATATGCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-10681b	103	T A ---	---	ATGACTCAGGTGACAAAAGAGCATGCTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAGACATCCTTTTAAAGAGCC[T/A]AAAGACAGCCATTTTATCCTAATTCG TAGTTTATGATTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAGGAGTGACGCTCTGTAAAG
WI-10681a	41	A T ---	---	ATGACTCAGGTGACAAAAGAGCATGCTCTAGACCCCATTTG[A/T]CTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAGACATCCTTTTAAAGAGCCCTAAGAGAGCCATTTTATCCTAATTCG TAGTTTATGATTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAGGAGTGACGCTCTGTAAAG
WI-7222c	126	G T ---	---	GCCTCTCCTCACTGCTCTGGACCCAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGATGG[G/T]AATAA AGGAGGGGAATTCCTTGAACAAGAACTGGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGGTTGATTTCAAGACTCGAATTCATTT

WI-7222b	255	G A	---			GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAGGGGCTGTGAGATGACTGTGGTCCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGATGGGGAATAAAGG AGGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGGTAAGGTTGATTTCAAAAGACTCGAATTCATTTTCTCA
WI-7222a	126	G T	---			GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAGGGGCTGTGAGATGACTGTGGTCCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGATGGG(GT)AATAA AGGAGGGGAATTCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAAGTTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41	C A	---			AAAGATGACACTTAGAACTGGATGACACTTGGCCCTTTCTCTTTC/AJTATCTCTCTCCAGTTCAAAATG CTTGCACTTTTAAAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTGATACGCGCTTTCCTGGGCGTACAGAGAAATCCTTGGCCCTT
WI-8054c	237	G T	---			AAAGATGACACTTAGAACTGGATGACACTTGGCCCTTTCTCTTCTATCTCTCCAGTTCAAAATGCTT GCATCTTTTAAAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCTTCC TGTCATAACGCGCTTTCCTGGGCGTACAGA(GT)AATCCTTGGCCCTT
WI-8054b	148	T C	---			AAAGATGACACTTAGAACTGGATGACACTTGGCCCTTTCTCTTCTATCTCTCCAGTTCAAAATGCTT GCATCTTTTAAAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTTCTTTGTAG(T/C)TTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTGATACGCGCTTTCCTGGGCGTACAGAGAAATCCTTGGCCCTT
WI-8054a	131	C G	---			AAAGATGACACTTAGAACTGGATGACACTTGGCCCTTTCTCTTCTATCTCTCCAGTTCAAAATGCTT GCATCTTTTAAAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAG(C/G)A CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTGATACGCGCTTTCCTGGGCGTACAGAGAAATCCTTGGCCCTT
WI-10854b	152	G T	---			TTCCACAAAAAATCTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGACGACGATAGTTAACGTCTGGTAAGTTTAT ACGGTGTGCGAGGCAACA(GT)GGAGAGGTACGGGAATAGTTCTACTTCTCTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T	---			TTCCACAAAAAATCTCCCTGGGCGGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA(C/G)GAGACGACGATAGTTAACGTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGGAGGTACGGGAATAGTTCTACTTCTCTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127	G A	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATTTCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTGTTTGACGCGAGTTGAGCCATTGTGACAGAGGCTGTTAT[G/A]GCCTT CAAAGCCAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTCTGCTGATTCTAGATAATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125	A T	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGGCCACAGGCCCATTTCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTGTTTGACGCGAGTTGAGCCATTGTGACAGAGGCTGTTAT[G/A]GCCTT AAAGCCAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTCTGCTGATTCTAGATAATTTAAA GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60	T G	TTGTTTGTGT GTGGGTTTT	TGACATTATAT AAACGTAAAA GAAAATGT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTGTGGGTTTTTTT[7/G]TTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G	AG	CCACCTGGGGC TCCC	TTCAGTAACGTGCAAAATAGGAACACAGAG[G/G]GGAGCCCCAGGTGGGACAAATCATGGCTACCCCC TCCCAACAGAACAGGGGGAGGAGGTGGCCCCCTACACCCTTTAT
WI-8170b	259	G A	---	---	GGACTTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAAGTGCAATCTCATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170a	204	T A	---	---	GGACTTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAAGTGCAATCTCATCAATCAGAA A/T/A/AAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC
WI-8172	136	C G	GA GACA	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCTCTAAGTCACTCTCCAATACTCCAGGTACATGGTGAAGAGTCACCTGTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTGGTAACTCCCTTTTATTAATAATTGTTTCTTGACAT A/C/G/AGTACCTTTACAGGTATTACATTTCTCTCACCCGTTTACA
WI-8183	56	G A	TGC	TGAAATAAAA ACAATTTCTGT	AGCAGGGTTTGAATTTGATCCCTTATTTTACATGAAATAAAAACAATTTCTGTTGC[G/A]GCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T	---	---	GCCTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAACCAAGCATGGGATTTGCCCGGAAAT ATTAGCGTTAAAGGAG[C/T]TGAGTTGAGTCAAAACACGGG
WI-8712	44	G A	G	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGGTTAGTGGAG[G/A]GAGATGGTCAGGCTTCCTG TTCCCTAACAGCAGAGCCCCAGCAACCTAGAGGGCCCTCACCTAGCCCTCTTAAT

WI-8827	22 C T	TCCCCTGGGAG	GGGATTAGGAT	GGTGCCCTGGGAGACTATGG[C]/JAGTGAACACTAAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCCTTAGTTCCTTCCTATCCACCCAGTCTTCT
WI-8833	51 A T	TCTTCCATGCC	CCTCACACATT	CTCCGGCTCTTAAAGCTCTGTAGACTGCTCTCCATGCCATTCCTG[A]/JTGCCCTTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACCTGCCCTGTGCATAAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTATGCCATGTGGTAAAGTTCAATTTTCAGTACATGGGTAACCCAGGCCCTTCCC[A]/JT TATATCCAGGTATGCTACAAAGTTCTTTTAACTCTTATCAGAAGTTATTACTGTTTCTTAGAGAG GCTACCAGGCTAAAAATTCACCTTAGTTGGTTGTCTAATGTCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC	CAACAGCCA	GAGGGACTTAACCTTTGGCTT[A]/JCCCTGCCCTGGCTGTTGGCTCTGCGCTTGCTGTTTGGTTCTT TCTCTTCTACTGGCTTCTTCTTTGCTTTGCCAGCCACCTATGCTGCTGT
WI-8853	79 C T	CCCGGCATTG	AGTCTTCCCTGA	ACTTTTCTTGGCTGAGCAACCTCATCATCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CATTGAGGATA[C]/JATGGAAGGCTCAGGAAGACTTTCATTCTCAA
WI-8865b	52 A G	---	---	AGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCAATGGTGAACA[A]/GJACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAAA
WI-8855a	42 T C	CACAGACTGA	GGTAAGTCCGA	AGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA[T]/JGGTGAACAACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAAA
WI-8895	32 A C	---	---	GTGCCACAACCTGGACACCAACCAACAGAAAT[A]/JCTCCCGTCCCTTGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACAGGGATGCTCCAATCGCTCTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTGTGAAATATAATAAACTCTTTCC AAGGCTCCCATGCTTGGATGTCACA[G]/JTTATGTCAAGTTAATAAAGATTTCTAAGTGTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTCAACGGCAGACCACAAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCCGTCTGCGTCTCAGTCAACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAATGTTGTATCAGTGCATATTCTATGGAAA ATTATATCTCAAGTAAGTACCTAGCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA[A]/JTTAGTATATAGAAATATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAATGTTGTATCAGTGCATATTCTATGG AAAAATTCATATCTCAAGTAAGTACCTAGCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28 A G	GTGCAGGAAG	AACGGCAGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGG[A]/JTCCTCCCTCCTGCCCTTGTACCCACATCCACAGAGCA GCCCTAGTCCAGGTGCGCCACTGCCACCCACGGCACAGGGAAACAGGCCCATGCTGTC

WI-12108	40 C T A T A	TGAAAAGGG TTAAACTCAA ATTTC	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTTCTGGAAAAGGGTTAAACTCAAATATC[CT]GAAATACTTTTCATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAATTTATTTAA
WI-5989	29 G A C A C A G G C A	CCACAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAACGTCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCGTATACCCCATATATTAC CCCTTCATGTCTAAAGAAGACATTTCTCTTAGAGATTTTCATTTTAGTGATCTTTAAAAAAAAT CTTGITTAACCTTGCCTCCATCTTTTCTTGGGTGAGGACACC
WI-12201	61 C T C T G C A T G	CCCCTGATCA CCTGCAATG	CCGACACATA CCTGGC	ATAGTCTTTTAGCCTTTTCTCTGGAGTGTATGTCCCAAGCCCACTGATCACCCTGCATG[CT]GCCA GGTATGGTGGGGGTGATGGACGTGGTTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31 A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTGAGGAGCCAGCTCTGACTT[A/T]CTCTCTGTTCTGTCTCTCTCCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCCTTATATAGGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57 A G C C T C	TGGCCTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTTCGTTTGTATATGATCCGAATGCTTGAGAAGAAACCCCTGGCTCGCTC[A/G]GCOCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92 A G T T	CATGCCCTTTA AGGATTAAGT	TCITTTCTCTT TGGTAGTGCG	AGCATGTAAGGAGCAGTTTATTGATTGGTATATTACAGTTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTAA[A/G]CCACACTACCAAAAGAGAAAAAGATTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C A A T T	GTTGAGTATT GTTCTGCTCAT	GGGAAGGCTG GTACATATTGG	TCTGATGTCATTTATTGGCAAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTGTTCTGCTCATAATT[C]CCCAATATGTACCAGACCTTCCC
WI-12326	25 G A C A	GACAGACTTC AAAAGCAATT	AGGTTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAAAGCAATTAC[G/A]CTTCAGAAATACAAAGTACTTAATACATATTTTCAAAC CTGTTTGCAATTCAAACAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63 C T ...		---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGGATATAGGAATTTTCAGCATATGTATTAT[C/T] TGAACATAATTTACAAAAGTGAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTAGC
WI-11305	87 C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAGGAAAGGACAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[CT]TAGGGCCACGGGAGGGTGGGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67 A G T T T T	GGGAGGAAAA TCCAATAAAT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAATCTTTTAAGCAGGGAGGAAAAATCCAATAAATTTTTTAA[ A/G]AAGGTTTAGCTATCCCAATGCTATTAATACAATGAGGTTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40 C G T G C C C C A	GGATAAATCA TGTGCCCA	ATCAAGCTTTG GGGCTCT	AGCATCTGCATCTCCTTTATGGATAATCATGTCCCCA[C/G]AGAGCCCCAAAGCTTGATGACAT TCTGTAAGTTACAAAAATGTATCTGAAGAAGTTATCTGTCTTGCC

WI-11352a	69	T C G	AGCAGAC ATAGTGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAGGAGAGAGAGTCATCTACATAAGCACAGCACATAGTGGAA AGT[C]GCTAAGTGTCTACGAGAGGTCAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGGCA CACTTA
WI-11371	84	C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCGTGA GCAC	TTAGCCCATGCTGTCATTTCGAATCACCTGTGAACCTATGAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTGAGT[C]GTCGCTCAGCGGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTTCGATGCGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTTGGCCTGATGGTGACACAGAGACTTTCATATCTGTTTAAAAAGTC TCCTCAGT[C]AGGAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGATAGATCAGC
WI-11388	88	C A A	TGTTGAAAT ACACGTAAC	TGCCTTGTATC CAAGTTAAAT	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGGAGCTCATAAAAAATTAAGAATGAATGTTTG AAATTACACGTAACCTAAGTTC[C]A]TATAATTTTAACTTGGATACAGGCATTGTTATGCTAAT
WI-11392	55	T G A	GGTTATGTGT CTTGAACCTTA	GTACATTACAG TGTTTTGTAAA	TTCTATCATCCATTAAATGGCAGGTTATGTGTTCTTGAACCTTAAATAATAC[T/G]CTTTTTTACA AAACACGTGAATGACTTTCTTGTGAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACGTGT CATACTCCTCCCCAGA
WI-11396	52	A T T	TTTTGTTTTG AAATGGTGT	AGCTTATTTTC ATATTCACCCA	AAAGAATAAGATGGCATTGTTTCAGTTAAATTTGTTTTGAAATGGTGTTTTAT]GATGGGTGAATA TGAAAAATAAGCTTACCTCATCCACTCTAAAGAGGTAGTTGGTGAATTTTGAACCGTTGTCAT
WI-11441	100	C A C	TCCCCACCAAC CAGC	TGCCAGGGCCT TATTTG	CTGTCAGTCTTTCCCAACTAAACCGTGAGTTCAGTATGCTGGCAGCACGCTGCTGTTCTTGGTG TATTCCTACTGTAATCCCCACCAACCGAG[C]A]CAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGATGAAT
WI-11466	26	C T T	TGAGAAGCCA TTTATTTTGCA	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTATTTTGCAG[C]T]CTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAAATAAACTTCTATTATCTATTTATCTCCTCACATACATTT CATGTATCCTG
WI-13364	35	A G	---	---	TTTTCTTTTGTGCTCTTTTTTTAGTAGAAGC]A]G]GGAACAGTTGTCAATACTACCTTCTGTTGG TCCCTCTTTAGACAACATACCTTCTTTTGAATGTAAAAATGTCA
WI-11276	41	A G A	GGCAGOCAGG AGCAGAC	TGACTGAGGA GOOGGTG	AGGCAACACTGCTTTTATTAGCCGGGCGAGCCAGGAGCAGAC]A]G]CACCAGGCTCCTCAGTACACATT CCCCACCCCTGCTCGGTGCTCCCTCACTCAGGGCTGGGCATGGAGGGGCGAGGTAGTCTGGAA
WI-12210	76	A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACA CTATTGCAT]A]G]G]GAAAAACATATGCAAACTAGCATCTCTCTAGA
WI-14186b	88	A G	---	---	AATGGTCTGTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATACGGTACAAAAATTACA GGTGGTTAGTTCATTACATG]A]G]TACAAATCATTAGAGTCTTTACAAGTCAATTAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCATTGAT GGAAAGACAC	AACTAAACCA CCTGTAATTTT GTACC	AATGGTCTGGTTTTATTGAGAAAGCTGTTGGTCATTTGATGGAAGACACACATA/C/TJGGTACAAAATT ACAGGTGGTTAGTTCAATACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTGGCTATAGGTCAGTGGTTCTAAAACTTGAGCTTGAAGAGAACACTTGTGGGGCTT/A GTTCAACATGGACTGATAGTCCCAACCCAGATTTCTAAGTGGTGGGCTGGG
WI-12345	37 C A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGA/C/AJCTGAACCCCTCTGCAAGTATTCCT TTCCTGACCAGCTGGCTTGGCAGCTTTGTGAGATTGCAAAA
WI-13416	71 C A	AAATTTTGG AAGTTTTTCAG	AGTGTATTATAG TTCAATGAATA	GAAAAGGCTGTAATTTTATTTTCAAAATTTTGGAAAGTTTTTCAAAAAAAATAAAATGACAAGAACA CATA/C/AJAAATATTGAAATTTATTCATTGAACATATAAACACTTAGCAGAGGAAGGACTTTTGTAT
WI-12310	46 G A	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTTGGTCTT AAA	TTTGAAGAAGATGCTGAATTTATCCCAAGTATAATTTTAAAAAGCT/G/AJTTTAGGACCCCAACATA TTTAAACATCTCTTACACATACAGAATTTTCAGTTTACAAATATCCAGAAAGGCAATTTTCTTAAGCAG T
WI-12086	72 C T	CCGGGAAAC TTGGATT	GGAGTCTTCGG GTCITGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAAACACGTTTCCGGGAAACCTTG GATTTC/TJCCAAAGACCCGAAGACTCTCCAAGTCTCACTGTTAGTAAGGTCAATTTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102 T G	GCATATAATTC TTTTATG	GGAAAGTCTGT ACAAATCCC	ATGCTTTCACAGGTTGATTTTGTAAAGAGTTTGTCTATCTATAATTTTATTTATTTGGCATAAAGT TCATAATATTCCTTTATGATCTTTTAAATATCTG/TJGGGGAATTTGTACAGACTTTCCCTC
WI-11585	79 T C	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTTC	TTAGAAGGAAGAAATAAAACACGGTAATGGGAAATCAGTTCAAGAGGTAGGAAGGAGCTGGGTT TGCAAAAACAAAA/TJCGGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAGAGCAGGGGTAGAGT TT
WI-11604	68 G C	---	---	TTAGTTGGTTTCTGAAACITTTATGCTGTTTATTTTAAACATAGGATGTTCCAGTTACCAGCATTTI G/CJAGAACTAGGGACTTTTCCATGAAATAATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTC TTGTTACTCTGCAGTT
WI-11614c	108 C A	---	---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCAGTGTGAAACTGCA/C/AJATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60 A G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGOC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAAGACTCAGCTGCTTG/AJGG CATGTTCCCAACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83 T C	---	---	TTGATTTTACTAAGGCTCTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAAATAAA/TJCTACTTAATAAAGAAATTAGCCATACCACATTTGTTCCATTGCTAC AAGAACAATTTGGCAATGA



WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAG[G/A]GATAAGGTGACAGGATAATATACT CAGATATTTTAAATAAATACTTAATAAAGAAATTAGCCATACCACATTTGTTCCATTTGCTAC AAGAACAATGGCAATGA
WI-11627	23	T C	CCITTCCTTCC ATTGTCTC	CAITTGCAACC CATCTCAAG	ACCCCTTTCCTCCATTGCTCTC[T/C]CTTGAGATGGGTGCAATGGGAAGTAAAGCAAAAGGG AGATGAGAAATACTGATGCCCTTTTGCTGCGCTTACTTCCATTCGATGTCAGTCCATCCATG
WI-11636	61	A G TCCT	GGACTTAAAA AGATCTGCTTA	AGAAACTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAATACTATTTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCT[A/G]TA TATCCACATAACTCTAGTGTACATAAAATATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTTGGTA
WI-11637	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCATTTCTTATGGTGGCAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAAATATTATGTTGCAATTGCTCATCTTACTCTGACCAT[C/G]ATAATCATTTCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C CTG	GCCAAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTGAGCAACTG[G/C]AAACTGTCCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATCTACTCTACTCAGAGTTCACACTCATATTTTCAATTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A AA	ATTGATTTTAG AAGGAACTGC	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACTGCAA[G/A]CTTTACTTGAGGACAAGCCTTGCTGCGAGTTGTTT AAAATGTCTGTAACAATCAGATTCAGCCTGGAT
WI-11680	55	T C ---		---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCCCTTTT[C/C]TTGCATAAA GGCTGGGAAGGTGGTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C AGGGACAG	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACTT	GTCCAAAGAAAGAGATACITTTGACATCTTTATCACAGCAGGGGACAG[T/C]AAGGTTGGCTTCTCTA ATGCCACCATCTTGTTTTCAGAACTTTCCACTTCGCC
WI-11702	69	C T CAGCAG	GAATAATACT GAAATAACCA	AGAACAACTT AAGCAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACITTTCAATAATTAATAATCGAATAATACTGAAATAACCCACAGC AG[C/T]TTTCAGTATAATTTGCTTAAGTTGTTCTAGAAAACACTGCTAATTTTGTCTTCTGCAGA
WI-11706	60	C T TTCTCTCT	TGGCTGGAAT TTCTCTCT	ATCACCAAAG AACAAATCCA	TGCTGATTCATCGCTTACCATCTGGCTGGAATTTCTCTTCTGTACAATTTATTGCTGCTGGCTG GAATTTGTTCTTTGGTGATTTGTCCTTGTCTGCT
WI-11709	105	T A TTCAGTTTC	AGAAGCTTGC TTCAGTTTC	TCATTTCTTCT AATTTTACGGG A	AATATCATCTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCCTTTTGGCATACTTCATC TTCCTCAGGACACAGAGAGAAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAAAATTAGAAGAAATGAAT GGCCAGATGGATGGAAA
WI-11710	103	C A CAGTCTCA	GCACCTAGCCT CAGTCTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCCAGCACAAACAGCCAGCCCACTCTAGACACGCCCTTCAG TCCAGTCCATCTGGCACCTAGCCTCAGCTTTCAC[C/A]CTCTCCCTCCCTCCACACACTCCTTC

WI-11715b	123 C T	AGGCTGGCTGC AGCTT	TCCCCATCCTG TGGCT	AGAAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAATGCATTACAACTGGT TGTAATGTGGCCACTATGAATCCCTATGTATAAGAGAAAGAGGGCTGGCTGCAGCTT[C/T]AGCCAC AGGATGGGGACTGGGAAGA
WI-11715a	49 A C A A A	GCACACAATG TAAACACAGAC A	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAA[C/T]GCATTACAACTG TGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGAAAGAGGGCTGGCTGCAGCTTACAGCCAC AGGATGGGGACTGGGAAGA
WI-11727	43 G C T C A A C A	AACAATCCTT AAACAACATA	CCTGTGGTTTG TGTTGCAG	CTGGATTTCTATACCTAACAATCCTTTAAACAACATATCAACA[G/C]CTGCAACACAAAACCCACAGGC AAAATGAAAACAGATGCCCCAGACAGACCCACCACATGGCACACAC
WI-11728	16 C G ---	ATCTGTGGTTT TCGCTG	---	TTTTATTATCAAACT[C/G]CAATTCATTTTCAAAAATGTAAGTTATCATCAGTCCCCATCCACTTT CTCCCATCTCTTATCTCTTCCACCCCTACACTTTCTCTCCCTTACAACCCGGGTTCCAAA
WI-11758	61 A G T G C C T G	GCCTCAGAA GTATTTCTAA T	TGATGGCCCT GTGGTCTA	TTTTTCTCTTTTATTAAAGTCCGCTATATACTAAGAGGAGAACTGTGGTTTTOGCCCTG[A/G]TAG ACCACAGGGCCAATCACACAGCTTCTTGATAGAACATGGAGATGCCAAGATCACCATCA
WI-11295	37 A G A A T A T A A	GGCTCAGAA GCTCAGAGA GCAAGGGAA	AAAAGTGCTCA TCTGTGAATC T	COGGCCTCACAAGATATTTCTAAAATATAATTTGCTA[G/T]TAGAGTTACAGATGAGCAGCTTTTCA CAATTAGTGATGCAACAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93 T C ---	GGCTCAGAGA GCTCAGAGA GCAAGGGAA	---	AGCACATGATATTTCTGCTGGAGTTTCTGTGAGCTCAGCAACAGCAGAGTCAGAGATTAAAGAAAT ATTATTGCTCTCTTTTCTCCCTT[C/G]GTGATTGTTAATTAGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G C A A C C T C T G	GGCTCAGAGA GCTCAGAGA GCAAGGGAA	AAAAGTGCTCA TCTGTGAATC T	CATGACAACTCTTTTATTAAATGGCTCAGAGAGCAAGGAA[C/G]CACACAAAATTTACAGTCTGA GTTTTGCGGCAGAGACCCCTCTCCACCTTTTTCATGCCCTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G A A C C T C T G	CCCAACTTACC AAACCTCTG	CGGTAGGCGAG GCTAAGC	TAATCAOCCAACTTACCAAACTCTGT[G/G]CTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAATGGGCAAAATCAITCAACACAAAGC
WI-11879	61 C A A G T A T A C A	TCATCTAATCT GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTAGTATACAG[C/A]AGT GATTTCTCTCTTTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCCTCTA
WI-12469b	91 C T A A G T T A A A	GTTTTTAATGT GGTATTAGAA AAGTTTAA	CAATTTTCAGA TTGCTATAGC AAAC	TTTACTAAATTTCCATTTCTCCCTTTTATAGTTTTTATGTGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATTTCTATTCTA[C/T]TGACAGCACAGTTCTTCAAAGTTTCTATAGACAAATCTGA AAATGGGTTCTGAAC
WI-11906	52 A G A T C T G A A	TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAAAGAAAGAAATCTGAAT[G/T]GAGGGAACTG CAGAAATTAACTTTCAGTCTAATTCAGAAATGCCAGAGTAAGATGAACCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CCTCTCTGAG ATTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCTAAATGGCTATTTGTGTTG GGTGGTCAAG[A/G]CTATTTCAGAAAATCTCAGAGGAGGACAAATGATAGTGCACACTGCAGCCAGCTCG GACTGGCTTGAAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAATTTGGCTTTACAGGAAGCATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACCTTTGTCTCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAACCTTCCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAAGGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAAGTACAACACTGCTTATTTTCTTGCTTGAAGATCAGATCTCTGGTTTATTTAA[T/ G]ATCAACATTCCACCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAT[A/A]AATAAAAAATCTGTAAACACATTTCTCATTTCTCTTACGA ATACITTCITTTTGATATTGCAAATTCATATGTCATACACAGAGGCACCTCCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCAACAAATTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTTGACCTTT GTGTTATTTCTGTTTCAACTAAGGA[C/T]AGACTTCAGAAAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTCAATTTGTAGGAAGGAACATTTTCAAAAGCCCCAA
WI-15488	69 C T	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGAAAGTTCTCACTCTGCACTATAAAAAAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAAATAAGATGGAAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC OGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACACATCCGT[A/G]GTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAAGGTAACTTTTCCCATTTTACAGACAAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCCTGCTTTGAACGTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAAAGTA C[C/T]GTGGGGTCTGATGACTTCCACGGTCACTGGGGATCCCAACAGAAAGGGAA
WI-11070a	110 G T	CAGAAAATCA GCCAGCTATCT	TTGGAGTACCT CTCTGCACC	ATGAGACCCTGCTTTGAACGTTTAAACGTTTGGAAATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGCAGAGAGGTACTCCAA GTACCGTGGGGTCTGATGACTTCCACGGTCACTGGGGATCCCAACAGAAAGGGAA
WI-12020	121 T C	---	---	AATCTTTTATTTCCAGCTGTTGAGACAGTATTTTGGGGCTGATTTACCTCTAGCGCGGAAACC AGAGCCAGCTATTAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATTT[C/C]CTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142	G A ---	---		CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATGGCTTATCTTCTGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGGAGGAGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGATTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-11076a	106	T C AGGCA	TCCTGCTCTGG GTATGTGAC		CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATGGCTTATCTTCTGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGGAGGAGAGAGAG GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGATTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-14263	49	T C GGCATATTCA	GGTTATTCAAA AATTAGTATGG GACA		ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[T/C]TGTCCTCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGGAGCA[T/C]TGAAATGGGAAGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAGCAAGTACCATTTTCCAAAGTATAAAACTCGTA
WI-14267	28	T C ---	---		GAATTTGTTTTATTCAATTCGGTTTTCAATTTTGCTTTTTAAATAGAAC[A/G]ATTTTGGATTTTAGTA TATGACATCATCATCATGAATTTTCTCTTACTTTGTTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGATGAGTTCA
WI-13892	50	G A TAGAAC	TGATGATGTCA TATACTAAAA ATCAAG		ACCTCTTTCTGATGACACTGTACCTGTAAAGGGTCTAGAGAAAGAGTAGTAGCTCTACTTTTGC TACAATTTCAGGATGACGGGCATGAGAGGATTCCTCTCTC[G/T]CCAAGGGAAGAAAGCTTTTGGC AATAATGGAAGAAGGAGTGAACAAAGTAATGAACAAACAGCCAGATCAGAGGAAGAGATG GCTTTCTTTGTTAATCTGAGCA[G/C]ATTCAAGCAGCAATAATTTACTGAACACTTGCTATGTGCTG G
WI-13951b	88	G C ---	---		AATAATGGAAGAAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCCGATCAGAGGAAGAG ATGGCTTTCTTGTTAATTCTGGAGGAGATTCAAGCAGCAATAATTTACTGAACACTTGCTATGTGCTG G
WI-13951a	39	C T CAAAA	TTCTCTGATC TGGGGTCT		GAGACCAAAAAAGGCTCTTGCCCAT[G/A]TATTCGGTCTCTCCCTCTGACTGACCCCAAGTGTCTT ACAATGAACATCCCTCAGCCCCATGGCATGGTGCATCCCCCTCTCTTGGGATCTGTGAATATAACCA ACTGCTTGTCATGGC
WI-13264	25	G A TTGCCAT	GGAGGGAGAG ACGGAATA		TTATTTGTCAATTAGCAAAAGGAAGTTAAATACTGATAG[A/C]GATGCAAAATTTGCTTTTCATGCA TTTGTGGAGCAAGTACTAATCTTGTTCACTGTCAATTTCCCTCACAAGGAGTTGAGCCCTAGATGAC
WI-13960	39	A C TGATAGA	CATGAAAGGA CAAAATTTGCAT C		AACTCTTTATTTAGCTAGCCCCAGTGACTTTTATGCATCTTATAACCAAGAGCCTTCAG[C/T]AG AGCAAGCTGAGCCAGAGGTTTATCACACTTTTGCTCTCAGGGTCCACAGGAACCGGCTTGCT
WI-15843	62	C T CAG	CTCTGGCTCAG ACTTGCTCT		

WI-13983	52	G A	TCTCTCCACT CCTTAAACCT	CAATACCTCT TAGCCAGTGG	TTGTGATCTGATTTCCGAAACATAGAAATCTCTCTCCACTCTCTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTTGACAGAATATGCACTCACTGACTTAAACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51	A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAAGATAAATAAGATGGACTTGCAGGTGTAAGAAATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTCTTTGCCAACTATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAGGCCCCGAAATATGAGTGAGACTCA
WI-14284	55	C T ---	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAAATCTT	ATTTCAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAGAGCCCTGTTCTATATGAAAGACAAACAGGTGGCCATACCTTGGTGGAGGGATA CCGCTGCTATCCCAGAT[G/C]AAGATTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T	CCCCACTAAT ACAAC	AAGTCAGTGGT TCTC	TTATTTTGTAGTTACCCCACTAATACAAC[C/T]GAGAACCCTGACTTCAAATATTATGAGAG AAATTAATCCAGGGAAATTTTGACAGAGAATAATA
WI-13529	42	T C	CACAAACATT TATTGAACAG	TCTATACACT CTCACTCTCTT	AAATATGATTCCATTCACAACATTTATTGAACAGTTACCAAT[C/A]AGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCCTCGAGGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A ---	TTACCA	GCTT	TTATTTGTCAGAAATTCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTAGGAAAGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C ---	---	---	TGAAAGGATACAGAAAAAATCAGCGAAGT[C/G]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTCCAGTTGTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A ---	---	---	TTTATTGTTTGGTAGAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTGCTC CTAGATTACAAAAGTCAAAACCAATTTCCCTTTGACGCCGGGCCCTTGAATCTGACATTTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61	A G ---	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTTTTCATTAGCTTGTCTTCAAA[G/G]GAC AGAGAAATAAGATAAATACCTTAAAGAAATTAATAGAAAATTAAGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G AAGG	TTAATACCTCT TGTGGATAA	GAAGACAAGC TAATGAAAAA CAATG	TTGGTTTTTAATACCTCTTGTGGATAAAAGG[G/G]CATTGTTTTTCATTAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAATACCTTAAAGAAATTAATAGAAAATTAAGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACATTTATTTAGCATGCAATGAAATTTATCTGGCAATAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[AT]AAAAATGTTTCTGAATGTGCACACTAGATAATATATGCAGAATCCTTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAA	TCCATGTAATAATTTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAGAGATAAAATTT/GJACCAAAAAATTAAGATTTTTTGGGACAAATTCACATGTTT AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGGGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[CA]/ATGGAATCTAACTGGCAGAG AAATCAAGACCGATGGTGAAATCTGGGGCAGCTTCAAAATTTCTGCTCTTAAACATTTTCAC CCAATTTTTCATTATGGC
WI-13857	28 A G ---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[AG]TACATTTTAGGTATCTGGCACAATTAACCAATGT CTGCCATTTTGTGTAGCTTTCATACAGTACAGATTTTCATTGATGTCGCTCCACATCTG
WI-15809	77 T G	TGGTTTCTGT TGTAATGOC	TAAGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAATGCTT/GJTTTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ---	---	---	TTAATCAGTCTGTGTCAGAAGAAACAGGACTTGATCAAGCTTCCAGCCCTACCACCTATCATCAGCA TAGCAATTTTAAGGATCAGAGCTTGTGTTTACATTTGTCTAAACCAAGAGAGAA[AT]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACCTCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCTTTTATTCGAAGATGGGAAGCG[AG]CATTTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACTCTA GCTGCAGTAATAC[AT]GJGATCCCATCCACTCTTCTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGCTCTCTCTC
WI-15801a	24 G A	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCTTTTATTCGAAGATGGGAAGCG[AG]CATTTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACT CTAGCTGCAGTAATAC[AT]GATCCCATCCACTCTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGCTCTCTCTC
WI-13763	59 T C	GGCTGGACACT GCAGTGAT	CCCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGATTT/CJAGGG GCAGGTGTGGGGCAGGGTGGGGCTCTGAGCCGAGGACAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48 T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTT GTC	TTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACCTT/AJAGACAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATGATATTTTGTCTTTTCCGAGGGCAAAAAGA GAGCTTCCCAGAAACCTC
WI-13789	62 G A	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTG	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACCTCAAGAAATGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGACTGGGGCTGGGACTGGAATATGGACAGTGGATGGTAGGGTCTCACTCTCTT GAGGTCCCT
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCTTTGGGCA GTACTTTT	AATAACAAGTTTAAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACACAGATCAAAAAAGC[ G/AT]GCACAAAAAAGTACTGGCGCAAGGACAAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40 C T	---	---	GTTCCTCCACCTACTCCCGCAGAAAAAGGCATATTCAAC[CT]GTCCCATACTAATTTTGAATAA CCTAACTCTCCCTTTGTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCACAG	TCCCCACCCCA OCT	GTCTCATTCTCTAGCTAGGCTGTAAATTTTCAGTTTAAACAAGTTCTTATGTGTTGGCCACACT GAAGACTCACAGAA[CTG]AGGGTGGGTGGGAATCTTAATCAATATTTGTGGAATTTACCCGAT GAATCCAGTTATTCCT
WI-13600	26 G T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACCTTAATGAGCCCAAGCATCCAT[GT]CCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGACCACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAGAAGAAATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTTCCATTCTGGAGACAACACA[GT]AAATCTATTATTAATTAATATTTGTCATGAGGTATGCACCT GCGCA
WI-13650	76 A T	AAAGATTAC AATATTTCACT TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAAAGATTCAATATTTTCAC TTTTAAAC[AT]TAAAAAATACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CAATCAAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTGAATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[CT]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAATT
WI-13528	80 A G A A A A	CAATACATTT GCATTTTCCCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTAAAAATGGTAGCTTTTAAACTGTAAATCAATACATTTGCATTTTCTTAAAA AAAGAAAGACATTT[AG]TTTTCAGAGAAACTGTGGTATCATGCAGGAAAAAGCAGAAAAAAATTT
WI-13909c	93 A T	---	---	ACTTAAACTGGCTTATCTTACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCCTCCTCAGACT CTCTTCAAAC[CTG]A/AAATATCTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCAGACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCCTCCTCAGACT CTCTTCAAAC[CTG]A/AAATATCTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A	---	---	TTTTTATTGAATTCCTCAATGTAGCAAAATCATTTAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAACATCATCTCGGAC[CTG]A/ATGGGAACCTTTGAAAGGCGATGGCAGTGGAGACCAAGTAACCTA
WI-14323a	78 T C A C A T C A	ACAGAAAAAT TAAGAATCAA C A C A T C A	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCTCAATGTAGCAAAATCATTTAAACAAATTTATAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGACCATGGGAACCTTTGAAAGGCGATGGCAGTGGAGACCAAGTAACCTA
WI-15389b	104 G A A A A	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCACACTT	AAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTTTTGGGAAGACTACCATTTATTTCAATTTATTTATGT AATACACTCATCCAGATAATGAACATCTGCGAAAA[GT]A/AAAGTGTGGGAATCACCTCATCTGTGTC

WI-15389a	33 G A T C	AATCAACTAG CTTGCTTTTIG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGCTTTTGTGTC[G/A]TTTGGGAAGACTACCATTTATTTCAAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAAGAGTGGGAATCAACCTCATCTGTGTC
WI-15747	88 T C A G T G T T	TGCTTCATTT AACTAATTT	CATAATTCACC AAAAGTTCATA TAATTT	TGTAATCTGCTTACAGTCCCTTGGCAAAGACAGACATATGTTTTGCATAAAGATATAAAATTGCTTCAT TTTAAACTAATTTAGTGTTTT[C/J]TTTAAATATATGAACCTTTTGGTGAATTTATGAAGTGTACCAAAAC C
WI-13752b	117 C T ---		---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACCTGCGAGCAGCTGAATGGCAGATGGT CTCTGCATGAGTTCCTCTCGTTAAGTGTGGATATACCTGGCTTGCAC[C/J]GGACACCTTTTACG GAGGGATTCGGACAAC
WI-13752a	106 T C A G T G T G G A	CCCTCTCGTTA AGTGTCC	CCCTCCGTAAA AGGTGCC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACCTGCGAGCAGCTGAATGGCAGATGGT CTCTGCATGAGTTCCTCTCGTTAAGTGTGGATATAC[C/J]GGCTTGCACCGGACACCTTTTACG GAGGGATTCGGACAAC
WI-14339	102 T G T T A C	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACACCTTCACTGGGTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACACCCCAATCAACACAGTACATGATTAGT[G/J]CGGTTTCCAGAAATCTGGATAC
WI-13744	115 C T A A A A C T G A A	TGGTGTGAAC GATAAGCACA	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACGTATGGAACCTCATGCAGCTTTAGAT TTCTTTGCCAGCTAGGAGCTTGTGTATGGTGTGAACAAAACGAA[C/J]GCTGTGCTTATCTTTC CTGATTCT
WI-14061	68 C T ---		---	CCTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAAGAGAGCCCCGTACATACCTTAT [C/J]AACCATTTTCATCCACCATTTGTAAAATCTCATCTTCTGGGTCTGGATACCTCAAAAACAGAT
WI-15719	69 A C C A T T C A G C	ACCTTTTCATC CATTCAGC	TGATACTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACTACACACTGAAATATACTGAATTAACCTATTCAACCTTTTCATCCATTGAG C[A/C]AATTTAAACTCTTGCCCAAGTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106 T C A A C T T	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAATCACACATAGATCAAAACAGAAAGTACCACAGTATGCTTTATTTTGCA GGTATTAAATGGTCTCTAAATCGATACATCCAAAACCTT[C/J]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27 G T C A C A	ATTTTATTCAC ATTAACCTTG	GTTCCTTGATA TGTCGCTTAGT TTT	GGATTTTATTCACATTAAACTTGCCACA[G/J]TAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACAATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA
WI-13785d	72 G A ---		---	TCAAACTGCACACTATAAAAGTGTCTTTAAATGCAGCAGGAGATGTGAAGACACACAAATGAAC AAGTGC[G/A]TAGTGACACATAGCTGTCAACACACAGTG
WI-13785c	56 A C ---		---	TCAAACTGCACACTATAAAAGTGTCTTTAAATGCAGCAGGAGATGTGAAGAC[A/C]CAAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACACAGTG



WI-13785b	40	C	---	---	TGTTGTGACAG CTATGTGTAC T	TCAAACTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAAATG AACAAAGTCGCTAGTGACACATAGCTGTACAAACACAGTG
WI-13785a	27	T	C	---	AAAAGTGCAC ACTATAAAAG TGCTT	TCAAACTGCACACTATAAAAGTGCTTT[C/J]AAAATGCAGCAGCAGGAGATGTGAAGACACAAAATG AACAAAGTCGCTAGTGACACATAGCTGTACAAACACAGTG
WI-13793	88	C	G	---	GGATTTTACAT TCAGCCTAGAT ATAGG	AGAAACCAAGTATATCATAGGCAATAAATAAGTTTTTACCCCATTTGATACAACATAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAATACTCTGCCATAAATCTATGACTTG
WI-13794	52	A	G	---	TTCTCACCCT TTCTTTCTC	TAGTCTCCTACAAATTCCTTCAATCCATTTCTTCCCTCACCCCTTTCTTCTC[C/J]TACAAGGTTAAGA GCCCATTCCTCAACAAACAAAAACAACATAGAGCAAT
WI-15729	35	A	G	---	CTTTGAACCAT GTGTAGACTGC	TCATTTAAGTGCACTTTGAACCATGTGTAGACTGC[C/J]GGCACTTTAGAAAAGAAGCTGAGACTGAA AAGTCTGTCTTACTTCCAAAGGAGGTAAAGTCCCTGTTTGAGCCCGGGGCTGCTCATTTGTTA
WI-13424	66	G	A	C	TGAGGTTTTTC ACCTATTCTT	GTCCCTTGACACAAGTCTCCCAACTGGTTTGAGGTTTCCCTTCTGAGGTTTTTACCCCTATCTTC[C/G/A] JTAGACCCCTGGGAGAAAAACACATGTGTAAGTGGCTCAGGACATAGGCAGGCCGCTTCACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29	T	C	A	CTTTATAAAA GGTCAGAGGC AATT	AACTGTCTTATAAAAGGTGACAGGCAATTT[C/G]AGATCCAGATTCAGCTTGCTCTATAAAAAGAT TCAACTTCAAGTAGCAATTTCTGTCTGCTTTTAAATCCTGAACATTCCTGAAGCACGAA
WI-13446	22	G	C	---	GCCATGTTCTT TCACTCATCA	TGCCATGTTCTTTCACTCATCA[C/G]CCTTCTGATTTTGTATCCCTTCTGCTCTGTAATTTTCTTCTTC TTCCCTTTTAGGGCCCTAGTCTGTTTAGAAATTCGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTT CTGACTGCCTAATT
WI-13725	56	A	C	---	TGAGCACATA TGGGTGOC	TCACACAAAGGCATTTTGAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTCAACAACTTGACCAGGCAGGTTAGAAGCAAGGCATGGTTCAGGATG
WI-15702d	107	T	C	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAAAT[C/J]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T	C	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]TCTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C	T	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]TCTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C	A A C A A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A A T G T T T T A T G A A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G T A A A G G G T G A G G A A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A C A A T A C T A A T G G G T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113 T C		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A A G G A G A T T C A C A T A C T T C C A C T G T A C C T C G G G T A A G T T T C C T C T C T T G T A G A T [G/C] G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A T C C T C C G G T A A G T T T C C T C T C T G T A G A T G T C C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62 G A		---	T G A T T G A G C T T A G A A G G A A G T C A T G T T G A A A T C A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G		---	C A C A T T T C A G C A A C A A A T C G A G G T G C A A A C A C A G G G T T A T T T C A C A T T A A T A T A A C T G G A T T T T T T G T C A A T A A A T A G G A [A/G] T T C T T T A A A T A C C A T C C C T C A C T T C A T G G C C A G T
WI-14373	95 A G		---	A G G C T G T T T T G A G G C C T G A G G A C C C C A A C A C A C G T A A G A C G T A A C C A T G G T C A T G T G A G T T A T G A G C T A G G A A C C C T G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C C A C C T C C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T	A A A G A A G T A A A T T A G G A A G A	T G T G T G C A T G T C T C T T A C T G C	A G A A C C G A G A A C T C A A A G A A C C A C A C A T G G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G A A G A C T T T A G A T G G T C A C G
WI-14083	47 C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A C T A C	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A C A A C A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31 A G	C A T T T A T T T C A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T C A T G T G T A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T A G T G A A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A A C A G A A C A G G A G G C C T T
WI-12169	121 G C	A A T A A A A C T T C C T A T T T C T T	G G G T C T G A G G T G A A A G A A A A	G T C A A A G G T G G C A A A T T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T C A T T T C T A A A T T T C A C C T T A T T G C T A A G T A T A A A A T A A A A C T C C T A T T T C T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T	T T G T T T T A T T T G G G A G A A T A A G A G G A G G G A G A T T T A G A C T G A T C [A/G] T T C T A G A G A T T T G A C G A C T A C A G C T C C T C T C T T T G T A C T A C G A G A C C C T G C T T A T A G C C C C A C A G G A A A T C C C T C A T C T G C G G T T G C A G A C A G

WI-14379	102	C T	TCTATTAAACA GGGTTATGTCA CACC	ATCATCTGTTT TGAGGTTGACA	TTTATGCTGTTGTTTCTACTGGTGGTCTCGCTCACTAATATCAATCCTAGTATGATTTCTTT TACTTGTCCTATTAAACAGGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[C/A]CCACCAATTAAACAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCCTCCGCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22	C A	...	...	ACCGCAGAGCTGCTGATTTAAAA[A/G]ACAAGCGTCTGGATCTCTGCAGGGGCTGGACCAGCTGC AGTGGGGGCTCCGGCACTGCTCTGCTCTCCAGGACTCTTCCACCAACCCC
WI-15937	24	A G A	CGCAGAGCTG CTGTATTTAAA G A	GCAGAGATCCA GACGCTTGT	TGAACTGAAACGTAATTTCTTCCA[A/C]ACACCGTAGAAAATTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGGGCAAAAGGAAGTTTCAGGTGATACAAGATGCTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24	A C A	AAACTGAAAC GTAATTCCTCC A	GGCCTTTAAGT TTCTACGGTG	ATGTTTTATGATCAATTTCCAAACATACAGTACAGGGAAGGTGAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92	A G	...	...	GACAAAGAGGCGAGTTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGGTTGACCT GCATAGATTTTTCAGGACTA[C/T]GTGGCCATGCCATTCTCTGAAGTGAATTTAATGAACA
WI-14125	88	C T	CATAGATTTT G	GGATGGCATG GOCAC	GTTTATTTCTCACAGTTCTGGAGGTTAGAACTGTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTAGGACTCTCTGGCTTACAGCTGGCTGCTTTCTCACCATGTCTTCACAT[G/A]GCCCAAAGAGAC AGAACAAGCTCTCTGGT
WI-14136	120	G A	ATGCTTTCACA A	CTTTGGGC CAGTATGTACA GTGACATAACA	TTGTTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCATTAATATTGTTTTCTTATGATTTGTTTCAATG
WI-14138	23	C T	GAAAAGCT A	TAGAACA GCTCATTTCTT	GGCAGGTTTATTCATAATTTTCAAAACTTGGAAAGCAACCAAGATGTCCTTCAGTAGTAGTATTTCA GACAATC[G/A]AATATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74	G A	GACAATC A	TAATATT	TTTTTAAAGAGTGCTCTCACATCAT[T/G]TATATTGATTGCACACAAAACTTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAAGCCTTCTTCAGAATCA CCTCC
WI-15953b	59	C T	...	...	TTTTTAAAGAGTGCTCTCACATCAT[T/G]TATATTGATTGCACACAAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAAGCCTTCTTCAGAATCA CCTCC
WI-15953a	26	T G A T	TTTTAAGAGTG TCCTTCACATC A	TCATCTGTTCT TGTTGTTTTG A	TTTTTAAAGAGTGCTCTCACATCAT[T/G]TATATTGATTGCACACAAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAAGCCTTCTTCAGAATCA CCTCC

WI-14631	82	G A ---				TGAATTCATGGACAGTTTTGCCTCTGTTTAGTGAAACCCCTCACAGCACTCTGCATAGTCCGCTTT CTGCTCTTTTAAAC[G/A]TGCCTGGTCCCTCTGCCAAACTTTTAGGATTGGCCCTCCTCAGGGCCTT GTCCTGA
WI-6053	24	A G ---				ATCACACCGTGTCTAAGAACAAC[A/G]TCTTCATGTCCAACATATCCCCGGGACTTTGTCAACTG CAGTACACTTCTGCAATTGAACCTGGCTTCTCTGGAGGAAGCCTCTAGAGCCAGGTAAGGGGGTGC AGCAGTGAGGGGTATATCTGGGCTGGCCAGTTGGAACACCGGAG
WI-15964	99	T A CTGGAGTA	GCTCTCTGTCC	GACTTCTCCAC	CTCTTTC	CAGAAACCTCTTCTGTGATTAAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGCGAGGCTGCCTT GGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTAT[A/G]CAAGAGGGTGGAGAACTTTGGCAAG
WI-12075	103	G A GGCAC	AGCAGCTGGG	CCCCTTCTTTC	TCCTCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAAGCAAGCCAGGCAATACCCCATCAG AGACAGTGACAAGAGCAGCTGGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGAGGGGAGGAG CCT
WI-12179	96	G A TGGAGTCA	GGAGGTACGG	TCGAATGACCC	TGTAGATGC	TAATTTAAAAACACGCCCTTCCACATAGTGCCTGAGGCATCTGCACATTTCTCTAGAGGACATGA ATAGTGATGTGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCAATTCGAGGAGGAACAG
WI-14651	49	C G ATTGT	CAAGAATCAT	GGAGATATTGA	CTTATTT	CACAAATAGTGAAATTATCTGAGCAAGAAATCATCTCTCAATTTAAATTTG[C/G]AAATAAGTCAGAA AAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
WI-14666	105	T A ---				AATGTGGACTTTCAACAAGGGTTAAACATAATCTAATAACAACCTTCTACAACACATTCAGAGCAT TATAACAAGAAATTTACAGGCAGCTAATGTATTAAT[A/A]AACCATGAAAGAAAAAATTTG
WI-13473	31	C T ---				ATCTAGATGTCAGCAAAATGGCTGAGACTGT[C/T]TGCTGGTAGATGCAGTGTGTGTATGTTCTAC TCTATTACAAAAATTAACAGAAATATGGCTTCGCTTTGTGCAATGTTTATATCACAGTC
WI-13967	103	A C AAATAAAA	AAAAGACTAC	TTGTGTTTCA	TG	AATTTAATAGCAGCTCTGTGTGTGATTTTAAAGAAAGATAAAATATGTCAATTCAGCAGTCATTT AAAAATAAAGACTACAGATACAGGAAATAAAA[A/C]CACTTTTAGGAGATGAAAACACAAA
WI-14408	60	T A G	GCAGACACAC	TTAATTGTGTA	TTACTTT	TTAATATTTAGCAAAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTG[T/A]AAA GTAACAAATGAGTTTTTACACAATTAATAATTAAACATACATTATGGGATTTGTGAATGA
WI-13683	47	C G ---	TATTACAGGCT	AAACTCATTTG		TTTTGTGTTAAGAAACAGCATTTTGAAAATAAAACCTATCTGCCCATG[C/G]TTTACAGCCTTTTAAAT TTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	C T CGTCT	CACCATGGCA	CATTGAGATAA	CAC	TTAGAAAACATGATAAAGCAACACAACCTTTTGGGAAAGCACCATGGCACGTCCTTTGTGCTA[C/T] GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A ---				ACATGGCAGATACAGAGCTGT[C/G]TCTTGAAGAACCAACCACTGACCAGGAAATGCCACTTTTACAA AATCATCCCCCTTTTCATGATTGGAACAGTTTTCTGACCCGCTCTGGAGCGTTGAAGGTGACCAGC ACATTTGCACATGCAAAA

WI-16002	59 T C	GATAACATAA AATGATCATG AGAAATTC	GCCATCTCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAATTTCA/T/CJGTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGGCT
WI-15361b	101 A G A	CCCACTTGAAC TCAAGTCATC	AAACTAAAG CTTTGTGCCTA AAA	GTGGAATTTTATTAAAGCCATCAAAATTTCCCTTACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCACTTGAAGTCAAGTCATCA/GJTTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAAACCA
WI-14759	73 T C	GGGTTTGACTT GTGGGG	TCCACACTGC OOC	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATTTGGTTTTATTCAAACCTTCTAGCGTTTGACTT GTGGGGT/CJGTACTCAATGGGGGCGAGTGTGGACGGGGGATTGCAACCCAGAGTTTCATACTG CAA
WI-12535	50 A T T A T	CTAGGAGGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCTAACATTTATTCAGGTGGTGAAGGGGTTGAGGTGTAGATA/TJCTTCTCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTGTGTTTATCAGCTGAGAAGGCGAGTCTCGCCATC TTAAAGACCTGCCCCC
WI-13805a	112 G A GGGAA	AAAGGCACAC GGGGAA	CTCAGCCTGOC TTGACC	TTCCATTTCATTATGCTTGGCTTTACCAATTTTTATAGCTATTGGGAGGCAAGGAAATTTTGGC CCAGAAACCATGAGATTTGGGTCAGAAAAAGGCACACGGGAA/GA/JGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T C ---		---	ACACAATATAATTCCTAT/T/CJCGAGTGATTAAAAACCTATTTGTTGTTTAGAACCAACAAAACTAC AAGAAAAACATTTTCAAAACCTTTTTTTTTCAGGCTGA
WI-14808	52 T A CTACCTGT	ACCCACACA CTACCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAACACCTTTAAGCAACAGTTAAAAAGTACCCACCACTACCCTGTT/AJAAAACTTTAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAAGAAACACAACTGAAGCCCCCATGTA
WI-14816	29 A T ---		---	AGTTAAAAAAATCGAGTCAGCATTTATT/AJAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCCCTGAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAAGCTACGACTTC
WI-12542c	71 G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/GT/JTAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/GT/JTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T TTTAAA	GCTATTAGGC AAACTGAACA TTTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T CAAAAA	GGATACAGCA GTAAAGAATA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTAGAAAACTGGGGATACAGCAGTAAAGAAATACAAAAAATCCTGC/C/JCTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---		---	TCITTTGGAGGGATAGAGGACAGAGTGTTC[C]GTTGATTTTCGTTTCGGTTTCAGTTTGGTTGTCATT GGTTTTTGTITTTTGTCTAATTTTGGCCCAACCCTATAAAAAGCAGTGCACCCAGAGGCAG
WI-14856	60 A T A A	TGGTGACAG GAAATACTT	TTTGGTTGCTA CTTTTACAAA CTTT	ACATTTCTTATGATAGCAACAATAATATGATGGATGGTGACACGGAAAAATACTTAAT[AT]TAA AGTTTGTA AAAAGTAGCAACA AAAATTTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAAA
WI-14863	61 G A ---		---	ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAAAATATTTTGTCTG[G/A]AG TTAATAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACATATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A	GACATCCAA GGCTCTCTAAC	TGGGGCTGCAG ACACTC	TTTTAATTAAACGTAAAAAGGCAGGACATTCCAAGGCTCTCTAACA[T/C]GAGTGTCTGCAGCCCCA TTGGCTTTGAGATGTGAATGTGTTAACCCAGGGTGGA
WI-14733	98 G A A	CCAAATTGAC AGATATTCTGC	GATGAGGTGAG GCCATTATT	ACGGAGTGGTCTCTGATGTATTTCTGTCAAAAAATGTTTGCCTGATTTCTAATCATGAAAGAACAATT AGAAAAATCCAAATTGACAGATATTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C ---		---	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATACAGGTGCCACTAAGGAAA ACTTCTCCATAC/AAGCTGCCTGCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCATCT GGCTGTGTTCTGTCTT
WI-14898a	50 A C C A	CATGTACAGG AAGAGTTGTCT	AAGTTTTCCTT AGTGGCACCT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATACAGGTGCCACTAAGG AAAACTTTCTCCATAAAGCTGCCTGCTGTGCACGTTGGCTGGGCTTTGCTAACCCCTGGTGTGCATC TGCTGTGTTCTGTCTT
WI-14907	48 G A G G A C T C T G A C	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC[G/A]ATTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACCCCAATCAATCAGTACTCCTGCACCTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52 G A C	CCAATACATT CAGTTCTGTT	CAAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCAACCAATACATTCAAGTTCCCTGGTC[G/A]AAGGTCCTTTTC CTGGTTGCAGACAGATACCTTGTGTATCCTCAGATGGCAGAGAAAGAGAGGAAATAATCT
WI-14913	88 C A ---		---	CTGATGCTTTGACATCTGGGCACTTGTCTCTGTAGAGAGACTACTTCTCTGGGACCAAGCAATTTTC TAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCAAAC CTACACCTCCAAACCCT
WI-14914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCAGGA CAATAAATTC	ATTTCCCTTGAATGGCTGCTGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTCTCTAGCA[G/] C]GAATTTATTGCTCGGGCTTGATGGCTTTCACAGC
WI-14926	49 T C ---		---	GTTTATTTTCAAAATGACACATCCAGATTGAAATGGGCACCTTAGCGAAT[C]ACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAGACAGTTTCAAAATAAAAAATTTCCCTTAATCAGGTCCA

WI-16083	89	C T	AAGGAT	ATGTTTAAACA CAAACATATC	TGGAAAAGATT OAGGOC	GCATCTTTATTACCAGAACTCAATTTATGTCCTTAATCATGTTTAAATATAATATAAGCATGTT TAACACAAACATATCAAGGAT[C/T]GGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAAACCATC CATTAAAGCAG
WI-14930	55	C T	CTCATGGAT	GGAGGAGTCC	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGTATTG GTTGGTTGGTGATTGGGGAGCACAGGGAGAGCAA
WI-14946	47	T C	---	---	---	TCAATCTGAAGGTGTCAAAGTGGTCTATTGGCCCCAGACATAACA[T/C]CTCTAAATCATCCTCTA GATCAGGGAGTCAATAGGACCATTAAGGCTCATACACACAGTACTTTATGAAAGGATT
WI-15987b	80	A G	---	---	---	ACATTAACACAGCACAAATTAAGGGTCCCAACGAGGTTGGTAGTGCCCTCCACTATGTGAGGACAC TAAGAAGATGGT[C/A/G]CTATGAACCAAGCTGCCGGTCCATGCTCTTAAACCTCTCAGC
WI-15987a	32	C T	GGGTCCAA	CACAATTAAA GGGTCCAA	GGAAGGCACTA CCAACCTC	ACATTAACACAGCACAAATTAAGGGTCCCAAC[C/T]GAGGTTGGTAGTGCCCTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56	T C	G	AGGAAACTG CTAACTTGTC	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTTCTTATTGCCGTTCTTCAGGGAACAGGAAACTGCTAACTTGTCAG[T/C]TCCAACA ACTGATGTAAGATCATCTCTGACCATAGOGAACCTGTAAAGGCTTGCTGCCCTCCAGCTGA
WI-16100	52	A G	TTGA	CAAAAAGCTA TTTCTCTACAC	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[A/G]GTAATATACTG TTTTCTGACATTCCTGTATCAACTCTCTGAAAATC
WI-14958	83	A G	CAAGGG	AATAATTTAT CTCTTTCTTT	AATGCATTCAT TTGGGTTTT	GTGATTGATCTGTAATATTGGGATTATTTATCAACTTAAATCCAAGATGAAAATAAATTAATCT CTTTCTTTCAAGGG[A/G]AAAAAACCCAAATGAATGCATTTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAAATCAAGGA
WI-14976	35	C T	TCGTTCAAAG	GTTGATTTGCT	TCAAACATAAT CTTCCATTCTA AGC	TATTTTAAATTTGATTGTTGCTTCTGTTCAAAG[C/T]GCTTAGAATGGAAGATTTAGTTGAGGAG GGGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAAGAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31	G T	T	TCAGTGGTGT TATTGGATTT	CACCTCTGACA TAATCTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT[G/T]TTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	C T	GAAGCTGCAG	TGCATTAAT	GCTATGTGCTC AGCTTCTC	TGATTACATTTTAAATCATGCCTACCAGCCCATCTAAGCCAAATCAAAACACCACCTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCAACTGATCGGAAAGAAACGTA
WI-15002	72	T A	---	---	---	AAATCTCTCTTTCACACACAGATGAACCTTAAATAAATTACAAATGCACCTGAAAATGCCCTTCTTGA TTTCC[T/A]TTTCAGTTTAGGCTCAAATGGCTCTCCTCAAGGCTGGACCTCAAAAGGCCAGTT
WI-15000	90	G A	GTCTAA	GACAGAAAA GACTCAGACT	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA[G/A]TGAAGTTTGTGCAGAACTAGAAAACAAAAATCCACCT

WI-12323	68	G A	CACA TACTT CATGTACCTAT	CACTGGACATA TTCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACTTTCATGTACCTATGAAATAA G/AJACAGGTAGGAATATGTCCAGTGCACACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A T A A C A	AAGGGACGAT TTAGTATCTAA	GGCATGTCCCA GTGTTTTT	CATAAGTTGCATTATTCACGTCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAAAACA/A/TCAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C A T	CC TGCCTTTAT ATTGGAATTC	GGGAGAACCATG GGTCTCT	ATTTGTTGTTTATTTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCTGCTTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGCACTCAGCCCTTC
WI-14712	38	T A C A	TGAATGCTTCC AAGTACAAAT	TGAAAGTATGT TGTATATGGTA	TTTGGTGCTACTTTTGTAATGCTTCCAAAGTACAAATCA/T/AJCTCACAATACCATATACAAACATACT TTCAATCACAACTCAAATATAAATAACCTACAAAATCACATTGC
WI-13712	40	A C T C T A T T G	TTTACTTTGTT GTCAATTTTAT	CCATAAGGTCT CACACTTTTCT	TGGGATACCCTTTACTTTGTTGTCATTTTATTTCTATTG/AJCTTATAAGAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGGCAATATGCAATAATAATTTGTGTGTTTAAATTTATGCAAT
WI-16163	35	C T A	TCGTGTGATGC AATTGAAATA	GC TGCCAATTA CATTAACTTAC	TCTAAGATTTTACTCTGTGTGATGCAATTGAAATAA/C/TJATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAGGTTAAGAGGACTATTCTTTAAACAAAGACAGTGTGACATTTATTTCAGGT
WI-13453	88	T A T C	AATGCACAAA ATCTTGCTCT	TCAGATTTTAA CATCTCTTCT	TTTTTTTATTGCAATTTGAGTGCCTTATTATATTGGGAAATTGCAGTGATATTAAACATTTGTACAAAT GCACAAAATCTGTCTCTCTC/TJATGCTAGAAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACTCATTGICCAT
WI-16167	58	T C G A T T T T	CGCACTCTAA ATTAGAGATA	TGCTGTGTGGT AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTCTGATATACATT/T/CJCATCTT ATTCAACACGAGCACACCCACACGACAGTAGAACAGTTCACACCTGATAAAATTGCACAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAAATAA/G/AJAATCTGCAAGTTTCCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAGAAATAAAGGACTGCTGTGATGTGACAGTCACTGGT
WI-15069	81	T C ---	---	---	TGTAGTCTTCAAAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTATTCCAGTATCATGTAC GCACTAAAAAAAAT/CJGTGTGCTGCTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C C C A G A G T C G C	TGAAGATTAA CCAGAGTGGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGATTTGTGTATCCCAAGATATACAGATACTCTATAAACCAACCCCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTGGC/CJCTCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59	G T A T G T	GCAGCAAGAT TACATCAGTA	CTCCAAATAGC CTAGAGTATAG	CATGGCAGCAAGATTACATCAGTAATGTAATAATAATACAGCTTTTTCATTGAAGCTTTTIG/TJACCTT TACTATACTCTAGGCTATTGGAGTGTCCCCAC



WI-15100	74	G A ---			---	TCATTACAGCCAGAAATAACCCAAATATTTCCAAATAAGCAAAAAATTGGAACAGACTGGA GTGAGAAC[G/A]GGTTCCACCACCAAGCCCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92	A T AATTACT			TAAGAC	TGGTACAGAATGTTTAATTACAGCAGGCGAGTGATTCCAGTTAAATAAAATTTAAACCTTTATTTT CCCAAATATAAAATTAATAATTAA[A/T]GTCTTAAAGAAAATATAACATGGTGACAGCTTT
WI-12002c	89	T C ---			---	TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACACCCAAAAACCCACATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[T/C]GCCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002b	68	G A ---			---	TCTTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACACCCAAAAACCCACATGGAGACAGAAG AC[G/A]JAGACACAACCTCTCCCCAC[T/C]GCCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002a	30	C G GGACACAA		TCGGAATCCA	TGGTTTTGGG TGTTTTCTT	TCTTTAATTTTATCGGAATCCAGGACACAACA[G/A]AGAAAAACACCCAAAAACCCACATGGAGACAG AAGACGAGACACAACCTCTCCCCAC[T/C]GCCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-15116	96	C T GTTGACGTAA		GGGAGCCCTA	CCTGAATATGC AATTAATTTAT ATGACA	TTTTCAATTTATTTCCAGAAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAAATTAACCTTTG TTCTGGAAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTCTATAATAATAATTCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-12578	37	C T AATGGGAA		GGCCTAAAGG	TCAAGCGACCA CCAACAC	GCAAAAGCAAAGCTATGGAGGCCCTAAAGGAATGGGA[C/T]GTGTGGTGGTGGCTTGATACCTTGGT GCTGTGTGCATGGAGCAGAAAGTCTTCCCTGGTCCATGCAGGGGGCTCACATATTTTAACTGCACATAAT TTGGGCAAACTGTGCTATC
WI-15153	40	A G GCATTGCA		CCCTTATGTTG	AACCTCAGATA AGTGCAGTGTCT	ATTTACAGTTGGCCAAAGATCTCCCTTATGTTGGCATTGCA[G/A]JAGACACTGCACCTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTACCATTTCCCTAA
WI-15215	84	G C TCAAATGGG		TGGCTTTAGAA	CCAACAGGGGA AAAGTCA	CCTTTGCTCTCTGAACCTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTGAGGTATGGC TTTAGAATCAAATGGG[G/C]TGACTTTTTCCCTGTGTGGTGGAAAACTCTGTGAGGGTTTGGCA
WI-15225	80	C T C		CTTGAGGACCT	TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGGTAAAGCAAAGCCGATCATTTGGATGGAATGATTATGTGTACAGCAGCACTTGAGGAC CTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAATTCGAAGTTGGAGATATGCTAAAA
WI-15152	51	G A ---			---	AATTTGCTAGTGCAAATGGACCCAGAAATTTGGAAGGGCTATGTAACACTACACA[G/A]TATGCACACCAC AGCCATGTGAGTGTACAGATGCTCTGTGTGCTTTCAGCTTCTTAAAAACACATCAAAAGGCTGCA
WI-15123	55	C T TAGGATG		TGTTAGTGACA GACAGATAAA	TTGCTTAAGGG CAACAGAC	TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACTCACTGGGGAAGAAACAGACATGCAACACAGATATAAACACAAT

WI-15182	49	C A	GCACAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACACTAGCTAGCTGCACAACACAGGGGCAAAATACATGCTGGATTAAACCC ATGCTAATGGGTTACCTTTATTAGTAATCATGGGTCCCTCATAAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGOCCTGGC ACTATG	ACTATCCGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTTGGCACTATGTCCTACTCTGCCTGACGGATAAGTTGGC ATATGGTTTCAGATTGCTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42	T C	CAATTTATTGAG TATTCCTTGCTT	GTGTAGTCTT ACATGCTTACG TAGAC	TCAAGTGGTAAATAGCCATTTATTGAGTATCTTGCTTTGATTTCCTGCTACGTAAAGCATGTAAGACT ACAACATTACGACCCCATCTCTTCAAGAGAGGAAGTCTGGTATTATGGAAAAACATTTTGTCAATTCAGAT T
WI-14510	104	A T	TGGCAAAATA TGCAATAACAA	TTGAAAATGGT TAAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTTAGTGTAAGTACACCCACAGATATTTTGGGGAAGAG TTGTTTGTCTTTTGTGGCAAAATATGCATAACAAAATATTTGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57	T C	CAATTTGCAAT AAACACCATC	GGACCTTATCT GTGGACTCAGG	CAGTGTATGACATTTCAATGGGAAAAAGATTGTGCAATTTGCAATAAACACCATCATTTTCCTGTGAG TCCACAGATAAGTCCCGGAGAAAGGGCTTCCCTCTCTCTCGCTGGTGGTGGTTCACCTCCCACTCCCGAGT GAAGCCTTTCTGGAATG
WI-12634	52	T C	GCATCATATG AACTGTCTAGC	GGACAAATTTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATTATTCGCTATTAGCTA TGTTTACAATTTGTCTGAAGGGTCTAGATGTGTACACCCACAGAAAGTGGTGAATTCCTGA
WI-15249	34	T C	GGGCTTGACAC AAAGTTCTAA	GGAAAGCCAG AGATTTTAAAC AA	TTTGTCTGAAGGGCTTGACACAAAGTTCTAACTTTTCCTTTTAAATCTCTGGCTTTCCTGGCTGG TGAGGAGGCACAGGCTGGGCTTTCAGGTATCCACTGTGTGCCCCGATCTGTCCCTCCCACTCCCGAG CCACATTTCTGGCTCT
WI-12159	28	C T	AAGACACCGT GCAAATGC	CCCTCTCTCA GTGCATTT	CTGTCCGGGGAAGACACACCGTGCAAAATGCCTAAAGTGCCTGAGGAGAGGGAGGGTCTGTGACTC CCAAACCTCGAATATTTTATGAATCTAAGAGTCCAGACGCGAGTTTCATCCACGGAGATCTGC
WI-12648	41	A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCAGATTGTATGGAATGCCCTAGTGGCATTAAAGGATGCATGAGGATGTCCACTTTTAGTAGC AACCGATGTTAATCACTACTCCATGTTAGGTGCTTTACTTGGATTATCTCAGTTAAAAACCAACA
WI-12684	64	G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAAACCATGCTGTAACACAGCTGTGC[G/ T]CCATTAGGCTTTGTTTCCATTTAGAGAGCACAGGAGAGGAAATTTAGCATAATTCCTT
WI-15260	75	G A	AAAGGATGAA GCTAATCATG	TCTCTCCAGG AGCTTGC	TTTATAAGCTGAATGAAGAGGTGACACAGCGGACACTGTCTAAGTGGAAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGACAAAATCAAGAATGAGCTGGAGAAATTA TCTG
WI-15325	39	T C	CATGTGGCTGG GAGGC	CCCTCCACCAT GATTGTGA	AAGGTTAATGGACTCACAGTTCCATGTGGCTGGGAGGCTTCCTCACAATCATGTTGGAAAGGCAAAA GGCACATCTTACATGGTGGAGTCAAGAGAGAATGAGAGC
WI-13936	123	C T	AGTTGGCATTC AATAGCCTAT	TGAAAACCTCCA CATGGAGTT	TATTTGAGTATTTTCATCCATGGGCTTCTCACTCCCTATACATTCCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTTCAGAACCTATGACCTGTATCTTTCAGTTGGCATTCAATAGCCTATCCTAACTCCATGT GGGAGTTTCATAATAA

WI-14528	62	T G T A A T	TTTTAACTTT TCTGGATGGTA	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAATTT/GJTT GAATTATAAATTTTAAATTTTATAAAGTGCTAATCGAGACATCAGTGGGTATAATTGA
WI-15347	74	C T A A T T	GACITCAAAG GAAAAGAACA	TCACTCCCCCA AGTCTTIG	TATTTCTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTCTCAAAGACTTGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-14546	95	C A G G A C T C A	CCAAITTTCTAG TGATAGTAGA	AAGGTGCACGT GCAGG	GTATTTTCTGATGCTTTGACATCTGGGGCATGCTGTCTCTAGAGAGACTACTTCTCTCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA/C/A/CCTGCACGTGCACCTTTTCATATACAGATCA
WI-15353	37	G A	---	---	TTTATTGGCTGTCTCTGTAATACAATGTGGTGAAAAAC[G/A]TCTTAAATTCAGGACATCTTCCACCTTG TTTTGGCTTCCAGTTGTACTGCAAGACCAAGTGTGAGGCACATAGGCTGATTAAATCAGTGG
WI-14580	100	G A G T C T G C A	CATTCCCACATCT GTCITGCA	CCGACCAAGAT CCCTDC	AGAAATTTTTCCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTTCAGAACTTCTCAAATAC CTAGTATTATACACATTTCCCATCTGTCTTGCA[G/A]GGAGGGATCTTGGTCGGCTTAAACA
WI-8540	73	T C G G C T T A	GGCCTGCATTT TGCTTA	GCCCTTCTTTT TCAGGCAC	CCAGCTGGAGGTGGAATAATGCGGCAACCACAGAAAAAACACAGCTACACACAGGCCTGCATT TGGCTTAT/C/GTGGCTGAAAAAGAGGGCCGACCTCTTGATAAAGATGCT
WI-8039b	97	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAAATGCACATCGCACATCAGAGTAAATACTG TTTGGTAAACCTTGTTCAGTTAAATATGTA/C/GTGCCTGTCATGTCATGATTAAATATCCTTCT TACCACAGTCACCCCTAAAGAACCAAGCTTAGGACTAGGACACAAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAAATGCCGACGCCACACCCACA
WI-8039a	87	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAAATGCACATCGCACATCAGAGTAAATACTG TTTGGTAAACCTTGTTCAGTT/C/JAAATATGATGTCCGTGCATGTCATGATTAAATATCCTTCT TACCACAGTCACCCCTAAAGAACCAAGCTTAGGACTAGGACACAAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAAATGCCGACGCCACACCCACA
WI-8044	107	C A	---	---	CACAACATTCAGAAGTTTCTGCATTGTCTCTCTGTATGTCTAAAAGATTTGAGCTTTGACTAT ACGATTTCCACACTGAACGATTCATAAGGTTTCTCCC/C/A/JAGTATGGATTCTCTGTGATTAATA AGCCCCGAATCTGGCTAAAGGCTTCCCACATTCACAGACATTTGTAAGGTTTCTCCAGTGTGGAC TCTCTGGTGTGCAAGAATGGAATCGGCTGAATGCTTTCCACACT
WI-8550	32	G A A T G C A A C A A G	GGGAACATCA ATGCAACAAG T	TTTGTGGCTTG AGTTTACAAT	CTTACTACATGGGAACATCAATGCAACAAGTA[G/A]AATTTGTAACTCAAGCCACAAACTTAGTTA ATAATCATGGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGA
WI-8057	87	T A	---	---	TATTAGATAAAACCTTTGTCCGATTCAGGATGTTTAAATTTGCTTCTCTTTAACTCTGTGACTTTT CCTGGTTCAAAGGACAGT/A/GATGGACAGCAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGCAAGGCACCTCTGTGGCTCACAACCTGCCCTGTGAGAGGATGCTGCCCTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG



WI-6375	28 A	GGTTATTGCA TATGGAAATC GAA	AATGTGAGATC TTTATTCTAAC CTTTT	AAGGTTTATTGCATATGGAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGATAAAGATCTC ACATTTGTAAGGCACATATGAACATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAATTCATAACCTTGTTTCTGATAAGACAAATTCAAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[A/G]CAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T	A ---	---	TTGTGCTCAACAGATGAATTCATAACCTTGTTTCTGATAAGACAAATTCAAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A	T ---	---	CTAATATAATCCTGGGCACATGGATCCAAGAGAGATTTTGCAGCAGATTTTCAATATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACATAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]ATCAACCTTCCCTAAGCATCTGTCTGTGTCGG CAGC
WI-6523	165 G	T CCTG	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCTGGAGTCCAAACAGGATGTGGACGTCCCTGGTAGTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCACAACAACAGCAAGCTAAACCTCTGAGAGAAAAAC[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C	G ---	---	ATTGTAATTAATAATTTACATGGCCCTATTTTAAAGGACATTTGTGTAATGTTTCCACTTTGTTTTAAA [C/T]AATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAAGTTTGAAAAATGGGCG
WI-6558b	68 C	T ---	---	ATTGTAATTAATAATTTACATGGCCCTATTTTAAAGGACATTT[G/C]TGTAAATGTTTCCACTTTGTTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAAGTTTGAAAAATGGGCG
WI-6558a	42 G	C ---	---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCATA[T/C]AGCAATGGATGCTGTGTCAGAACATACCTGCCAATAAATTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGATGTAAAGATTATGGAAGAT ATCGTGAGCCAAAAAC
WI-6629	75 T	C GTCATA	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAAAACCTCCAGCTGTTTCTCTGCTTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAGAAAGTCAATTTCTCAAGCACA[ T/C]ACCAAACTTGAAGGTGATTGAACCCAAAATAATGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGGTTATATTTTGATGTTGCCAAT
WI-6644	134 T	C ---	---	TGCTAAACACCACCATTTAAGGAGAGTACTAGGAAAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACAGC[T/G]GGCTAATACACTGCAATATTTTA TGTTAGCAATATAGCTGGTCTGTGTATTAACCAAGAGAGGGTATCTGG
WI-6690b	106 C	T AGCCACAGC	ACATAAAATA TTGCAGTGAT TAGCC	

WI-6690a	28 T	AAACACCACG ATTATTAAGG C AGAG	GCTGTGTTGG TAGTTTTCT	TGCTAAACACCACCATTTAAGGAGAGTCJACTAGGAAAACTACCAACACACGCGCATGTGAAAC AGTTGGGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACAGCCGGCTATACACTGCAATATTTTA TGTTAGCAATATAGCTGGTCTGTGTATACCAGAGAGCGGTATCTGG
WI-6770	53 A	CAACCCCAA AACATCACA	GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTCCCAAAGTAATCCAAACCCCAAAACATCACAAGJAATTAATTCAT ACTATTATACACTCCAAAGCAAAATACCTCAACTGCAATCC
WI-6686	151 A	GCAATCTTCCA AAACAAAGA	CCTGTAAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTGAGCAAAATCAGTACGCACTAATCTTGACCAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAAATTTAGATGAAATTCACATTTAAACATGGTAACCTCCAAGCATTCCT TCCAAACAAAGAATAGJAACATTTGGAATAGTCACTTACAAGGAC
WI-6761	32 C	GATCTAACAG CTGCAGAAATG C A G	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGAGATCTAACAGCTGCAGAAATGGCJACTCTCTCCCTCCAGCTTTTGTGAACAAAC AATCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTTTCAGGTACAAAGTCTC
WI-6844	225 T	---	---	TAAATACTGCCAACTAGCATTACGTCCACTCTTGCAATCAATTAACAAACAAAGGTTATTCCTCTTG GTATTTCAAATGATGATTAACAATAAACGAAAGTTAGAACTTAAATGCACCTGATTAATATG TAACTGGTAATTTGTTTTAAAGCAATAAATTTGGTCTCTTCTCATAAAATGGAATTTTAA TATTTCTGATAGTCTTGAGGTTCJATCATTATGAGTAGTGCAAGTGTG
WI-6824	112 A	---	---	CGGTTTGTACACTTAAATGGTTTTTTTTAAGGATTTTTTTCAGGCTTTGTGACAAACATCAA ACAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCCAAAGJACACCTTAGAAAAATTACAT GACCGGAGAAATGCGCTCTGCTCTGGAAGAGCTTACAGTCTAGGATTTGACAACTCACAGT CTTAGGAAGTGGGCAAGTAAGGCAATTTCTATCCCTAGAGCTATTGTG
WI-6889	139 T	GAAAAATGAG ATGCAGTTAA C AATTC	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAGCTGAGAAAGAGGCAACATGGAAGTGTCAAGAAACATTCGTAGGTACGGACAA AAGAGCTCCTTCAATCAAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTCJ/CJAGAATAATTAAGGCCACAAAGTGAACGTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T	---	---	TCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACCTCAAAATATCTGATGAACCTGATGAACGAA AAGAGGTCTCCTTAACAAGATATCATCTCCGGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTGCCTCCCAAGGAATGTGTTCTAATTTGGTTTCAAGCACACTGGTTCC CACTTTTACCACCTT/CJCATGACATTGGACAATAGTACTACTCTTTCTAC
WI-9413	112 G	---	---	GCCAGTCTCTAGTAAGTCTCTAGGGACATGACCAGACCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACCTGGGTGGAGGATACCGCTGCTATTCACAGATGJCAAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAACAGAGGTATGA
WI-9557	74 C	---	---	AAAAGCTTTAAAAAAAGTGGTGTCTCTTTAGAAACACTTTTCAGCAAGATCAAGTAGCCCCAGCT ACAGCCTCTGGTGCATCTTAACCCCTCTCCTTTT

WI-9617	37	G T	---	---	TGCTCTTTTATTACGTTTCACAACACACGCCGTG[GT]GGCAGCTACCAAGTGCCCCGAG CGCCACGCTTGGCCGGAAGTCTCATTCTGTCTCTATGGAGTATTGAATTTGGGATGGCCAG CTCCAGAAATGTTCCACGTGGGGGACTCTGTGGCAGAGAGGCTGAGCCCTTGCCACACTGGCACCA AAGAGTTGCACGATGCAGTTGCAGTGGTCCAGCCGGGTGTCTGTG
WI-9657	121	T G	---	---	AATGCTGGAGAAAACATCAACATTGAGTTGACATTGTTTTGCTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAGT[GT]GATAATCTTT TGATTAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTGAGG
WI-13119b	114	G C	CCTCCCAAGTA GCTGGGA	AAAAATTAAC CAGGTGTGGTG T	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGATGT[GT]CACCCACACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGCTCCTACTATGTTGCCCGTCTCAAAAAACAAACCAACTAAC CAGGGCTTGCTCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT[GT]GACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGATGTGACACACACACCTGGTTA ATTTTTTAAATTTTGTAAAGATAGGCTCCTACTATGTTGCCCGTCTCAAAAAACAAACCAACTAA C
WI-13119a	51	C G	---	---	ACAGGAATCTGAAAGTTACCAAGGAAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[CT]CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACACTATGTCACAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71	C T	AGCTTTT	GGAAAAAG	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[GT]AACACGATCAGTAGTGACACITTTGAT AAAAAGGAAATTTTAGCTTAGTAGAAAGAAAGCCCAAGGTGAGAGTATAATGAAATATGTACAT CTTTATGGAACCTGTTTGTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-12988	36	A	CTCAGTACAA	GTTT	TGCTATTTCATGACAGACACGCTGAGACAAATATCTTATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGAACCTGAGACTTTA[GT]ATCTGCAAGGGGTTTAAATAAT GCAATATCACATATATTTCCATTTTAAACACCATAATTAAGTTTCCATTTCTTAATAGAAAAATGA TAAAAATGTTTCCCAATAT
WI-13020a	108	G A	CTTT	CATTATTAAC CCCTTTCAGA	TGTATAAAAAATCCAACTGTTCCACAAGTACATATGCTCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAGTCCAA[GT]TACAAAAAACAAGCATTTCTCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGCGGATGAGGCAGAAAGCA AGTGTGTTT
WI-12837	87	A G	AAAGTCCA	ATGCTGTTTT	AGTGTGTTT

L42611b	50	G C ---				GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCTGTGTCGTCCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGGCCTCAGCTTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATAATGTATTCAACCA CTGGAGCTTCACITTTGTAC
L42611	34	T C ---				GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCTGTGTCGTCCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGGCCTCAGCTTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATAATGTATTCAACCA CTGGAGCTTCACITTTGTAC
WI-1172b	179	C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG		TGAACGTGTGGTTAAACTAGGCAATTTGGTTAAATCAATTTAAACACAGGCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGAGTGAAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C A ---				TGAACGTGTGGTTAAAC[C/A]TAGGCAATTTGGTTAAATCAATTTAAACACAGGCCTAGAAACA GTGACCACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGAGTGAAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35	G C A	GCAGATTGGA AGTGTGAAAA	CACTTACATTT CTGAATATTTA GACTCTTT		AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTGAG AAATGTAAGTGTGCTGCCCTCACTGTTCTTTACCCACTTAATTTCTGCAATTTTGAACACTAGATTGAAT TCTTTGCAAAACCCCTTGCAATGATACCCGAGTTAAACCGTTAATTTAAAGACATTAAACATGG CCTGGTG
WI-1231b	141	G A ---				TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGGTTCACAATAAACACATAGGCTCTTTATTTCTCCCTTCTTTTCAATTTTCTT TCAC[G/A]TTATCCCTCACCCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAATCCACTTTAC ACATTCGGACC
WI-1231a	126	T C A	GGCTCTTTAT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA		TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATTC CAACTAAGCAGGAGGTTCACAATAAACACATAGGCTCTTTATTTCTCCCTTCTTTTCAATTTT CTTTCACGTTATTCCTCACCCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAATCCACTTTACA CATTCGGACC
WI-472	114	G C ACAGAAAAG	ACATACATAT CCATTATACA	GACCTTTCTTT TCCAGGCC		GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG[G/C]GGGCTGGAAGAAAG GTCAAGTGAGATTTCAGATATTTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT



WI-478	46 C T T G T T C	GCATGCTGTG T T A C T C T A T T T	AAATGCCACAG G T G G C T	AAACCACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTTGTTC[CTAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATCTGCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAGGCTACCATCAGTACCTTAGCACATTTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T C A A C T	ATCAGACGAG A G T A C C T T T C T	CCTTCCAACCT C T A C A C A A T C T	AGCCATCACAGCAGAGTACCTTTTCTAACTT[CJATAAGATTGTGTAGAGGTGGAAGGAGGACAGGA CTGTTCTGTTGGTATAATGACCCCTGTGTCCAGTTAATCCA
WI-601b	112 T A ---		---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAGAGAGGTTTCATTGACTCCTAACTGAGTAC[T/A]CAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T ---		---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAG[C/T]GAACAGAGAGGTTTCATTGACTCCTAACTGAGTACTCAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G C C T C A C C A	CTCCTTCACAA C C T C A C C A	CTTCCCGGTAA G C C A A G T	AACAAAACAGACACCCCTCGGCTTCTCTCACCAAGTCCACATGGTGCCAAACAATCCCACATTCCT ACATCTCCCACTGGCTGCTCTTCAACAACCTCACCA[A/G]ACTTGGCTTACC GGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTGTGCTT G T T G A T T T A A T	TTATTCTAATC C C A C A T G A C A G	ACTCACTGCTGCTTGTGTTGATTAAATCAACCTAGCC[G/A]GCTGTGATGTGGATTAGATAAAATA AACACAAAATGAAAACACACAGATTGCTAACAAAGCAGATCTTTTTTCAAGGCACACGTAAAGAT AATAACTTCAA
WI-991	37 A T ---		---	TGCATTCATTATGCACCAATAATAACTTCTGTACAT[A/T]CATATTGATTTCATTATCACAAAAT TATGAGTGAGGGATGATTGTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTGACAGAGCGGGATTCCGAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAAACACTGACTCCTTTTCTCCTTTGAAAACAAGGC
WI-1011	70 G C C A	CAGTATCTGA A G T T T T G T C T	AGGAACACCTA C A A A A T G A C T T	CTTCTGACCTGTTTGCAGTGGATAGTGTTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTTGTCTCC A[G/C]JAGAAGTCATTTTGTAGGTGTTCTCGGGGTTTTTGTCTACGTTTTCCATTTTCTCTAATACACTGC CGTCTTAAGGGAGGGCTGCAGAGCATTTATCAGATGGCTGTTTGTCTGCAITCTGTGCACTGAAG
WI-5381	178 A T ---		---	TTTCATGCAGAAAGGTCCATGAGTTTACAGAACTCAAGGAAGAAAGGCCCTTAGAGATGACACCAGAA ATGAGAGTGGCTTGTCTCATGAAAATTGGACAGCATGTTCCAAAGCAGGGAACAGCATGGAGAAGA AAAAATCATCTATCCACGTGCAGAAACTGGCAATTAGTTTTGT[A/T]TTACTAAAACACAAATGT TTAACTTGGGGTCCACAAACAAGGATATGTTGGCAATGGTATTCTGTGATG
WI-5791b	76 G A ---		---	CTATGTTATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAAAAAGATGAGAACAGGTCTTA GAACCTCAG[G/A]ATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCCAAAAGGTA AAAAAATAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTTGGCCACCCTGTTTGT TAGGAA

WI-5791a	44	C G	---	---	CTATGTAATCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTT[C/G]ACAAAGATGAGAACACGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCCAAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTTGCCACCCTGTTTGT TAGGAA
WI-5406c	120	C T	---	---	CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGCAAGGTGAGAAAC[C/A]CCTATGAGCCAC ACTTCTCAATTCCTTAGAATTTCTTGGAATCTGTGAAGAGGAAGGAAGAAAGAAAGAGAGGCAA GG
WI-5406b	118	C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGCAAGGTGAGAAAC[C/A]CCTATGAGCCAC ACTTCTCAATTCCTTAGAATTTCTTGGAATCTGTGAAGAGGAAGGAAGAAAGAAAGAGAGGCAA GG
WI-5406a	42	A G	---	---	CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGGCCACTTCCACAGATGCAACAGGCC GGCTTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGCAAGGTGAGAAACCTATGAGCCAC ACTTCTCAATTCCTTAGAATTTCTTGGAATCTGTGAAGAGGAAGGAAGAAAGAAAGAGAGGCAA GG
WI-5798	48	G C T G	TTTATTCCTCC TTGTTTTCTTT	ACTGTTAGAAA ACCAAGTATTTT TCAAT	CCATTCTCTTCTCCCTCTCCCTTTATTCCTCCCTGTTTCTTTTG[G/C]ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T A T T	TCTTCATGAAT TCATCTTTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTTAAGCAGATTGTCTTCATGAATTCATCTTTCAGTTT[A/T]AGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAAG	TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAAGAG[C/T]CTTAAACCATAATTTTGTTTA GAACTCCTGTGCCCAACCACCTCTTGATGTGAGTGAC
WI-5481b	131	A G C T G C A G T C G	TGTCATTTATG	TTACTTCCAGG CTCCAAGTATT	AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCAATGGGCATCTGTTTCAAG TCTGTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG[A/G]A ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5481a	29	G A A A T T	CCAAATTCAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGATGAATTT[G/A]AAATTTTACAGTATCTAATGCAATGGGCATCTGTTTC AACTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5492	38	T C	---	---	TCATGAGTCTTCTCAAAGATGCTTGTAAAGTCCCAT[C/G]CAAAAGAAAGGATCCCATGGCCTAAT GAAGATGACCTCCACCTTAGGATATTTGCAGACCAA

WI-5826	134	T C	---	CCCAATACITTT TTCAGGTGAA	---	TATTTTTTTTCTCAATCCTGGAGCACACCATGCTCTTTCTATTTCATGCTTCACATTTATTTTTT TTTCACTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGCCAGTTTATACATATTTCTTTAGTC/C] TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCAACAGCCAAACAGCCTCACTCTTCCTT CCTTGGTGCAITTTACTCTTTACAC
WI-5546	40	C T A	GGCACCAGCCT TTTTAGAGT	CCTGTATTTTA GCAACATGGG	---	CCTTATAACCCCAATACITTTTCAGGTGAAAAAGGGAAA/C]TACCCTATGTTTCTGCTAAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATACAAATGCTTGAGTGTAATCTGATGTGGGAAATAT TAGAAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	GGCACCAGCCT TTTTAGAGT	GGCACCAGCCT TTTTAGAGT	CCCAGG	TGTTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGTTTTGATTGAGCGGGTATGGGT GGGGCTATCGGCACACGCTTTTTTAGAGTC]TCTGGGCAATTTGTGCACTAGTGTGAGA
WI-5836b	161	C T	---	---	---	TAAAGTGATTTAAACACTCTGTGCTCAATTTTTCACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGTGGATAGACATGAATACTCTGATGATACTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCATGATTC]TCCATTTTGAAAATTAAGCTTTTGAATTTTTCCTCA ATG
WI-5573	58	C T	GTTCAATAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC	---	TCGGGTATTAGGATGCGTTCAACCTCGATGATGGGCGTTCTAAGAGGTGGGA/C]T]GACAC ATTACTCTCCAACCTGTTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A	---	---	---	CAGGACCTTGGAGCCTTGTCTGTTTGTCTTCCACCCCTCACTCTTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCCCTCTATGCACGCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTC[G/A TTTTGGCAATTCCTGTATATCAACAGAGAGAGGAGGTTGG
WI-5850a	92	C T	---	---	---	CAGGACCTTGGAGCCTTGTCTGTTTGTCTTCCACCCCTCACTCTTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCCCTCTATGGA/C]TGGCTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCGTATATCAACAGAGAGAGGAGGTTGG
WI-5612b	125	A T	CTATTAATGA GCATCGTGCA TTC	TTCTCTTGAGA AACCTAAAC ACTG	---	TGCCTGATTGACACATAGTTATCTGACAGTAATCATTTCAACATCACAATAATCTTATTTCTGCCTG TCACACTAATTTGCAAGCATTCAATTGATTGACTATTAAATGAGCATCGTGTCAATTC]T]CAGTGT TTAGGTTTCTCAAGAGAAATTTATGCTGTCTTCTCTGTAACCTCAAGTA
WI-5612a	44	T A	---	---	---	TGCCTGATTGACACATAGTTATCTGACAGTAATCATTTCTAACAAT]A]CACAATAATCTTATTTCTGC CTGTACACTAATTTGCAAGCATTCAATTGATTGACTATTAAATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATTTATGCTGTCTTCTCTGTAACCTCAAGTA
WI-5636	26	A C	GCCAAATTTAT CCGCAATAAA	CATCGAGGACT TTGGGA	---	TGAGAGCCCAATTTTATCCGCAATAAA/C]T]TCCCAAGTCTCGATGGAGGCAATTCAGAAATCGGG GCAGGGGAGGCAAGGTGAGACAGATGTGAAGAAC

WI-5865c	103	C G ---			---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAATTAAC[G]AAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTCA GAGAAGACAGACAACATAAATAATTCAGG
WI-5865b	99	T A ---			---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAATTAACAAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCCCTCA GAGAAGACAGACAACATAAATAATTCAGG
WI-5865	165	T A ---			---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAATTAACAAATATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAATGACCAAGACACAGT[A]CCAGTCTCCATCTTCAAAAGGTCACAGTCCCTC AGAGAAGACAGACAACATAAATAATTCAGG
WI-5874	76	T G ACAGAAAA	CATAGCATGG ATAATATTAT		CCTAGTAAGTT TCAGTCAATTTG ATATGT	CTCAGACATTCATTTTCATTAGTTGTTAATTTTGTATTTTCATAGCATGGATAATATATACAGAA AAAAATTT[G]TACATATCAAAATGACTGAAACTTACTAGGTAGCAATTTGTTTGCAATTTGCT CATGGAGCCGACGTTTCAGCTCTCAGTTTTTCCATC[A]TTTTTTCATAATTTACTCTCTTTCTGTC ACAATGTTCTGCTTCGTTATTTCAACTCTCATTTGCTGATGGATGGTAGTCATAAAATATGGGTGATTC AGAAAATAAGTAAATG
WI-5752	36	A T TTTTCCATC	CAGCCTCTCAG		GACAGAAAAAG AGAGTAAATT ATGAAAAA	TTAGCAGAAAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCGATAAAATC[G]C CATTAGGTATTAGATAAGCATCCCATAAAAACATTGTTGAAAAACGAAGCCGAGTTTCGATTACACACA GTTGCTGTTTTAACCTCTCTAAATCCCGATAAATAGCATTAGGTATTAGATAAGCGTCCCACGAAA CATTGTTGAAAAACGAAGCCACGTTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5760b	61	C G ---			---	TTAGCAGAAAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCGATAAAATACCCAT TAGGTATTAGATAAGCATCCCATAAAAACATTGTTGAAAAACGAAGCCGAGTTTCGATTACACACAGTT GTCTGTTTTAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCG[G]ATCCCACGAA ACATTGTTGAAAAACGAAGCCACGTTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5760	187	G A ---			---	AATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG[A]GTGCAAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAGGTGAAGACTACTCATTTCTCAGICTTCTGCTG
WI-5944	52	A G GGAATCTTG	TTCTCACCATG		GGGTGGGATCT AACTTGCA	GAGTTTAATGAATCCTGTTCCCTCTAAAAACCTCCTGTTCCCCCAACTTCACATTTCAGCAGATATT CTTTCATGGGTTATTTGCCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGGTGTGAG TAATGCTTGGTA[C]TTTTGCTCTGTGCCGTATCTGCTCCCAATCACCCCATTCACATTTATTTCTTATTAT GCTGAATGAAACGGTTATATTACAG
WI-5967b	148	C T ---			---	

WI-5967	165 C T ---				GAGTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCAACTTCACATTCAGCAGATATT CTTTCATGGTTATTTGCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGTCTGTGCCGTATC/TJTGCTCCAATCACCCATCCACATTTATTCCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53 G C ---				GGGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GCJGTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGCACGTGAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTTCAGCAAACTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA		TGAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAATAAATGAAAAATTGAATAATTAAAGCACATTCCTTAATTAAAGCAT CTACAAGGTACTTAT/CJCACTGTTCTGGGGTTTCAATCCTCTTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAACAGGATTGTTACATGCAGAGAAATAGGGGAGATAAAATTTGTCTTTT CTC
WI-6450	45 T G TGTCACA	CCAATGACTT ATTCTATATCT		TTGTTTGAAT GTGTGGTACTT CT	ATAGGACAGTTTTCTTCCAATGACTTATTCTATATCTTGTACAT/GJAGAAAGTACCACACATTTCA AACAAAGAGCCAGGCTATGCCAGGGTGGGATTATTTCAACGGTCACTGTAATATGCATGTAAAGACTA TTTTACTGGCTTCTTTTATGCTATAAAACAGGATTGTTCTATTCAACAAACATGTGTCAATACAG CAGTTGTCATGCTCCTCTGGTACTAGATATAGTCTTTATAGAATATGTGGTTTAGAATAAAGCCACA AATTATCTATAAAACAACA/CJJAAGGAACGAGGCTCAAAAGTGGAAACAAACGGCCTTAGTTTC TAAGTGGAGACTAAGACGATATAGGAAATATAATCCGTGACCTCTTA
WI-6461	88 C T ---				GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATTCTTTGGTCACACAGGACTTTCTGGGCT ATGAAATAGTCTATTCAGTGAAGTATGTTATCATAAAGACATGCAAAACCTTTTCACAGTCTTTGT CCTGG/GA/JAATATCTCACAAAATTAATTAAATGGCATGGACTTTCTGATTTAGCCTGACAGG ATTGTTCTTT
WI-7466c	141 G A TTTGTCCTGG	TTTTCACAGTC		AGTCGCATGCC AATTTATAATT	GAACTATCCTTTAGTGGTGCCACATTTCTATTCTGATTCTTTGGTCACACAGGACTTTCTGGGCT ATGAAATAGTCT/CJATTTCAGTGAAGTATGTTATCATAAAGACATGCAAAACCTTTTCACAGTCTT TGCTCTGGGAATATCTCACAAAATTAATTAAATGGCATGGACTTTCTGATTTAGCCTGACAGGA TTGTTCTTT
WI-7466b	80 T C GTC	GACTTCTGGG CTATGAAATA		ACTGAA	TGCTTTTAAAAATAACAATGACCACCCTGACACCATAGTCTGCTCCATTTGCCACGTCTCCTC AGTAGAATAAGACAGGACTTTGCTGGCTGCTATCT/CJATTCTCCTTCAGAAAGACACTTGGCCCT CATAGGCATTCATAGATATTGTTGAATGAATGTGCTTTTTCATATTGATTCTCCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9814	104 C A ---				CCTCTAACAGAAAACTTGACTTCTCCTCAACTCAAAATACCCTTCTCTAATAATTTG/JAGTAACCA AAATATTCCTTCAAAATAAATTATCTTTTAATTAGAAGCAACAGTGTAGAGGTAGTACATTCA CCAOC
WI-9720b	55 A G ---				

WI-9720a	47 A G ---	---	CCTCTAACAAAGAAACCTTGACCTTCCTCAACTCAAAAATACCCCTCTCTA/GJATAATTTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTAATTAGAAGAACCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---	---	CACGCTCTAAGCAGGATGTGGCTTATGAGATACTTTGCATTGTCTGCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTGCATGTGCAGATGAAGGCTCAGGGTCTA/TJGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTAGTTTGCATT TAAGAAATGCCAGTCTTTTGCTGCTGCATCATCTTGAACATTATCCACATG
WI-9748	74 C G ---	---	CCACTTCAGTAAATCAATTTGTAGCACCTTATTTCTAAAGATTCTAAATTTTATATGTTTACCCTTT GTCATT/C/GJTCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTCTGGAATCTTTTCAGAAT TACAGTTATGATGCTCTTTTATATCCCA
WI-9943	91 T C ---	---	TGAGGCTATGATGCAGATTGTAGTGACTAATACTTATTAAAGCAATTTCAATGTTGTGGGCACTGTT CGTTGTGTTTATATCCATCTT/CJATTTTAAATTTCTACTGAGCAGAAAAAAATGTATACATT AACCTTTGCTCCCTATTGTACCTTTAATATGCAATTCACACCTTCTCTTTTGTCAATTTAGGGA
WI-9891	39 T C ---	---	AGGGCCCTTCACAGATCCGTCAGCTCAACACTGCCTCTT/CJAGTGAGCCTGTGAACCCACCCAAAGAC GGCTGGTCATCAGTGCATCCTCTCTCTTCCGGACAACTATCTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCAATAATCTTGTTTAAATAATCTTATTAGGCCAAATCCAAAT GTGCTGAAATATCTGCCAAGCATGTCAATCTACACAAAAAGGATTGCAAA
WI-9897b	84 C T ---	---	CTCAGAAATATTCAGATCTCCCCAAATGTCATGATTCTTGTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGT/CJJAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---	---	CTCAGAAATATTCAGATCTCCCCAAATGTCATGATTCTTGTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGT/CJJAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCACACCTCACAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGGTGTGGACTGGCAGGGGGAGTTTCAGACA/CJAAGCCAAAGAAAGCC TGATATTAGAGGCACCTTGCAATTA
WI-9935a	42 C T ---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTTGCAC/CJACCTCACAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGGTGTGGACTGGCAGGGGGAGTTTCAGACACAGCCAAAGAAAGCC TGATATTAGAGGCACCTTGCAATTA
WI-9983	146 C T ---	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCTCCCAATTCCTTTGTCTTGA TTCCCCAAACCCCAAGTTCTCACCCCAATCTGATCAAAATGCTGACTAGGTGATGGCTGGTCAGGGTAA AGCATTTATGA/CJJAAGACACAAAGACAAAGAGGTTAAAGTTGCTGTCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAAGG

WI-10019	139	A T	TGATGTAATGC TATGTAGCAA ATCT	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTTGAGTATACAGCAATCTATTTTGTTTATTTATGTGTGCTATAAATCAATGGTCTTA ACATTCAATAAGATCTTTTGCTTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAAT CTA/TATCCCTTAAGCACAGTAAATCAAGGCCCTTCTACCCCA
WI-10020b	122	T A TTT	GCGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTTTT/AJAAAAATACC AGACTAATGATTAAATAAATTAAACAGTCTAGGGTTCCGGAAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10020a	39	T C A TAAAT	TGTCATCTGA CTCGATTAA ATAAAT	AAATTCCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTATTGGCGAGAAAAGAAATCATGACTTTTTTAAAAATACC AGACTAATGATTAAATAAATTAAACAGTCTAGGGTTCCGGAAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10064b	170	C T TTTACATG	CCTTAGATAT ATTGTGATTGT TTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGTGGTGACACTCTGTTTATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG/C/TJGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C A CAGGGAAGG	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG/C/AJATTATAATA AATAAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGTGGTGACACTCTGTTTATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T C CAAACTCTT	TCTCTGTGCCC CAAACCTCTT	ATTCTGTGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCCAAACTCTTA/T/CJTAAATTCATTCAATACAACAAGAAATTTATAGAA TATGCACCACATGCCACAAGACACCCCTTATATTAGT
WI-1319	40	A T ATTCTTT	TGGCACTTAG AACATAGTTT ATTCTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTCTTTT/AJACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTTAGGTCCTGTTTATAATTTGGTATCTTTTGGCACAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTTAACATTAACACTGGTCAGATGTGTTTAAACCTGTTGAACCTGCAGC
WI-10316	104	T C CTCTT	CTGTTGATTTT CTACCTCTATT CTCTT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACITAGTGAGGTAAATCAGAAGCATCTATATTATTCACCAGTCACCAACCTG GACTATAGTCTGTTGATTTTCTACCTCTATTCTTAT/CJTAAACCTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAGGATGTTTAAAGCCCGCC
WI-2572	61	C T ...		...	AGTGAGTTGTCACAATTTGGAGACATCTGTGACCCCACTTAAACACACTCTCTCCACAC/C/TJAC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

WI-10368	31 C T	TGAAGCAACC AGTCTTGT	CAAGATATTAT ATTTATTCTCT AAGAGGGG	GAGGAAGTGCCTGAAGCAACCAAGGTCTGTGTT[C/T]CTACCCCTCTAGAGAAATAAATAATATCTT GAGATAGGGAGGAGCAGCCTGAGGACAGTCTGGGTTTGTCTACCCCACTGGAAGCAGAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGCCTTTACGGG
WI-10391	32 A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CTCCCGTTCTCTGTCTCAGGTATGACTCCCA[A/G]TCAACTTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTCCAGGGGAGCATCTGACACAGCCTTTTGCTTGCTGTGACAAACAGAACATTTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCCTCTAATA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTCTCAATAAATATTATCTTTTTCATATT TTCCAAATTTAATACTAGAAATTTTCAACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGTCTT CTAATAGCAA[A/C]AGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	...	...	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTCTCAATAAATATTATCTTTTTCATATT TTCCAAATTTAATACTAGAAATTTTCAACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAG TCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T C	GGTGCTCAAT AAATATTATT CTTTT	AAATTTCTGTT GGTGAAATTTT TAG	AGCGATGAAATTTATATGTTATGCCTGACTAGCGGGTCTCAATAAATATTATCTTTT[C/T]CAT ATTTTCCAATTTAATACTAGAAATTTTCAACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	CAAACTCAA ATTGCTTTAAG TACTTTA	AAATCCAACA GTCAAGGTCTT C	CGTTGGGAATATTTCTATCTCACCTAAATTTATG[C/A]GTGATTAATAATACATTTTAACAAACTTC TTGCTTTAAGTACTTTA[C/G]GAAGACCTTGACTGTTGGATTTTGGATTTTTCATTTTCTTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A	GGGAATATTTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATATTTCTATCTCACCTAAATTTATG[C/A]GTGATTAATAATACATTTTAACAAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGGATTTTTCATTTTCTTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C	CACAAATGTA ACAAGAAATTG ATCC	CCATGGCTGTA GTCCAGT	GTTGTGAAACTCCAGTATCATTTCCCTCAAAACCAGCTTAATCACAATCAGCTTTTCTTTCTGTA GAGCTCAAACTCAGTCTGAATGAAATGCTGCACAAATGTAACAAGAAATGATCCTA[T/C]ACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAAGGAAACACACACAAAAAGTTTACCAGTGAATATGACCAAAATGAGA[C/T]AAAT TTGTTAAAAAAAACCTCAAAATGAAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTGT ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTTCTTTTCTTTTGT[G/C]CTTTA GAAATCCATTTTGTCTTTTGGCCAGCAATCCCTCTCCCCATATTTTAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGCGGTACTATTACCCCATGGGTCAT AGAGAGGATTAAACAGGGGTGATGCCTGCAATGGGAATATTGAAAAACC
WI-10656	59 T G	...	...	



WI-11169b	154	T G T T T T	TTAACCAAGA G T T T T C A T T C	CTA A C T T A A A A A T C C T C A T T C A A A A T A T A A	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATAAAGCTAAAGTAGTGCTTTTAAACCAAGAGTTTTCATCTTTT TTTAAAAAAGAGCAGACAT/GJT/TATCATGTGTTCTGATAATTTTATATTTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95	A G T T G A A A A A	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT T A A A A A G C A C T A C T T	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATAAAGCT/GJAGAGTAGTGCTTTTAAACCAAGAGTTTTCATCTT TTTTTTAAAAAAGAGCAGACATTTTATCATGTGTTCTGATAATTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A G ---		---	CAAGTCTGGACCTTGGATAGGTC/GJACCCGGCTGAAGTTGGACAGTTGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTTCTTTGGGTTTACCACTAGGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGCTAAATAATCCAAAATAGCCATGGGTTTGGACAAAATAC AAGTTAGTGTCTCTAATCTAATGGGCATA
WI-10686	133	C T A A G G	TGCCCCGTGTC T A A G G	CAATCTCTAAA T T C A T G T G T A G A C A C A	AATAACCTGTGGCACATAAGGCAATACTGAGCCCCATACAGAGTGTTTATGTATATATGAAA AAAGTCAAGAGAACAAAGATATAGTCTGCTAGATACTTGAATCTGATGCCCTGTCCAAGG C/TJTGCTCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAGGG GGTAGGATGATCTAGAAATGCCACTTTACAGCCACTGAATATATGCTCCCAATGATCTTTCTG CTCAAAAGAGT/AJTTTTTTTAAAGTTATCTACTTATTTATCTGCTTTTCAAAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATAATTAATAAGTAAGAAAAAGAACCCAAAT TGGGC
WI-10694	144	A G T A G T T T C	TGCAAAATGCTT T A T G A G T T T C	GGCATTTTGTA A A G G A G G A A	TAGAGAGGCTTTTCAGTTTCAGGTTGGAGGGTGGTGAGGTGAGATTCATCTTAGAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAAAGAACTCAGTTCTAAAGTGTTCAGTCTTTGCAAAATGCTTTA TGAGTTTTTC/GJTTCCTCTCTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGAAAGCTTTCT T
WI-2716	23	T C C	TGAATTCATCC A G A A A A A C A G	TCTCTTTTCTC T C T T G T T G T C A T T C	GTGAATTCATCCAGAAAAACAGCT/CJGAATGACAACAAGAGAGAAAAAGAGAAATAAAGGTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTGTGTCCTCCAGTGCATGGAGCAGTG CAGGCCCCAACTCTGTCTAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAGTTTCTCTGTATGT GCCCCACCAATAACAGTTACTGGAGGATGACTCTCAAGGCCATTCATGTC/GGCTGCTGGCAGTGCTT TTCAGGCTGTGCCCCATAACTAA
WI-10719	115	T C G C C A T T C T A G	TGACTCTCAAG G C C A T T C T A G	GCACTGCCAGC A G C C	
WI-10721	40	A G C T T G C C A	TGGCTCTGCTA C T T G C C A	GAACTOCCAC A T A A A T A A A T C T C A	CAACCAATTCAGATTTAATTTTGGCTCTGCTACTTGCCCA/GJATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCTCTCCCTGCTTAGGTTTGAAGAAGTTGAA

WI-11204b	88 T C ---			GCACACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTTACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATATTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAGGG TGAAAAGAAA AATGTACATAA TACCTTT	TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTT/AJCACCTTTTATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATATTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTTCAC	GCTGTGCTTC CTGTATGTACA CTCT	AAGAACAATG CATAACAGAA CTTTAA	ACATGTATTTCCTTTAGTGGTCAGCCTTCTTACCCCCAAGAATATCCCTGGTTTATTGCTGTCTTC ATTGGTTCACCT/CJATTAAGTTCTGTTATGCATTTGTTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACCTCTGTTTAAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA CTCT	GAGTGACAATC CTAATGGTTGG	TAGTCTTTTCTTTGTACGAGTGTCTATAAAGAATTACCACCTCTGTACATTTTGTAAAAGATAGCACAG AGAGAAGCATTACAGGGCACACACAAACATGAGGTGTTGTTTCTGTATGTACAACCTC/AJTCCAA CCATTAGGATTGTCACCTCTCATATATAGACAGAATTCAGTGGTGGTGAATTTGAATTCACACACATGGA ATAAGTCTA
WI-11215	68 C T ---			GAAAAAAGTTTTAATTGGATTGCTTAGTTGCTTAAATTTGACCTACITTCAGATTATTTTAGT [C/JATTTTCTCTATAATTTCTGTAAGTGATGGATTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTTATCCAAAGCCCCATTCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAAAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAAATTGAGAGAATATTCAAAAAGTAGAGAAAA GAGACAAAGAGATGAAAAATAGGA[G/AJAGAAAGTGTAGAAAAATTAGAGGCCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11219a	18 G A ---			ATGAAAAATGCATTAGAA[G/AJAAATTGGAGGATAAAAATTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAAAGTGTAGAAAAATTAGAGGCCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11222b	136 G A GCGTGG	CATACCACCTGC AGTTGTGA	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAAAATGCTAAAAATTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCGTTGAACATTTGTTAAACATTTACCAGCATACCACCTGCGGCTG G[G/AJTCACAACCTTGGCTACAGGAGGAACCTGACACAGACTTCGTAATTTGCTTTACAGGCTACTGG AAAGCC

WI-11222a	25 C T A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTCG	AGCCACAGTGGAAATCATTTACACTA[C]TJGGAATCAGCAATGCTAAATTTGGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACCCACCGTTTGAACATTTGTTAAACATTTACCAGCATACCACCTGCGG CTGGGTACAACTTGGCTACAGGAGAACCTGACACAGACTTGTGAATTCCTTTACAGGCTACTGGA AAGCC
WI-10775	39 C T	TTTATGCCATA TTAATTCATTA CACTC	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTATGCCATATTAAATTCATTACACTC[C]TJACATCATATTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGATATTCCTGGCAGATAATCATTTGTTATCATTAGACATTGCA GGAACCCCATATGGATGATAAATGTTGTTTAAATGAAGGCAAGCAATTA TTGCATGCAATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATAGAAAAATGTCAGTGGTTGC TAGTACAGGAATCAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATATTCACAAATATAT TTCATGA
WI-11226	165 A C	GCAAGGGAGG AACATTTACA G	CTGGTGACATC AGAGATGGAC TTGAGGGACCC TGGGA	CAGTGGCTGGCTACTGACAAAAACGTAACTCGTGGCAGGTGGCAAGGGAGGAACATTTACAG[A/G]G TCCATCTCTGATGTACCCAGCAGGGCCAGGAGGTTGATCTGGAG TGGGACACACTGCTCTAGACC[C]TJCCAGGGTCCCTCAAAGGTGGGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGAGGCATCAGGGCCTTAGTCTCTCTGGGACAGTGAAGGGCCACCAOC ACAGAAAAATGCCCTAGGCTTGTAGCAAGAGAGGAAAGCATCTTCATGGGCAGGAATTC[C]TJCATTT CTGTGTTCTTAGGGTTTGTGGCTGGCCATCAGTTCACTCAGCCCTGTCCTGATCCAGCAACATT TCCGTAACCTACCCCTTAGAAGTCATGCAAGAGAAATGATGA
WI-10810	58 C T	CATCTTCATGG GCAGGAAT	CAAACCCCTAAG AAACACAGAA ATG	GGACCAACAGAAATTAATCTGGCA[C]JAGGGTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATTTGGATACATTAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10828	23 T C		---	TATGCCITCCCACAGGCCATCCACGCTGCTTAGCACAATAAGATAACATCATCTGAATG GGCACATTAATCTGCAGGCTCTCC[C]GJTTTCTAAGTCACCTGCAGTTAGTCTGCAGACACTGTGTA TACCATAAATCTGATTTCTGAGCAGGAGGAGGAGGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTCCG
WI-10832	91 G C	CATTAATCTGC AGGCTCTCC A	CCTAACTGCAG GTGACTTAGAA A	GATTGAGTATTATCAAAATGCCCCAAGACCATTAAAGATTTAATAGTTAAAGCCAAACTATA AAGAAATTAAGTCTCAAAAGTGTGTTAAT[C]TJCTTAATACCAATTTATAGGGCCACCATTAACCTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT GGATGATGTTCTGTGGTCCCTTTAT[C]JAAAGCCCTTGTGCATCCCCAAATGTGTAAATTTATTTCTCT TGGTATTTCTGCTTACCCTAGTACCTGTCAAGTGTTCACCCCT
WI-10834	96 C T	AGAAATTAAGT GTTCAAAAGT GTGTTAAT	TGGCCCTATAA AATTGGTATTA AG	
WI-2287	24 T C	---	---	



WI-2906b	77 T A ---			---	CCTGAACACCTGGAGCAGCTCCCTCCCTGGACACCTTCATCTTCTGGAACTTGCCTGGAATGCTCTTCCCTCT[GA]GAGCTTTGCTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA
WI-2906a	50 A C TCTTGCTGG	GACACCTTCAT		AGAGCATTCAG GGCAAGT	CCTGAACACCTGGAGCAGCTCCCTCCCTGGACACCTTCATCTTCTGG[GA]CJACTTTGCCTGGAATGCTCTTTCCCTCTGAGCTTTGCTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA
WI-1736	175 C T ---			---	TACTCCTCATTCTCATGTCCTAGACGTAAGTTCATGCTCCCTGAAACATTTATTTCTTAATTAGATTTCCACCCCGACACTATTTACACAGAACAGCATGGAGCAGTTTGGAGCTGGCTCTTAGAGAACTTAAAGACAGTGGTTTCCATCTGTCTTCCA[CT]AGAGATCTAGGGTGTCTTTGGAAACCACCTGG
WI-1851	136 G A GTGTTAAGTA	GCATTGAATT AACTATAGAT		CACTAGCAATG TTAAACTGAAG TTG	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTAAACATATTAACTGGGGAGGACACAAACATTTAGACCATAGCATTGAATTAACATATAGATGTGTTAAGTAATTATTAACATGGTACA[GA]ACAACTTCAGTTTAAACATTGCTAGTGATTCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62 G A AGAGACCCC	CCCAAAACAC		GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCAGCTGCTTACATCTCTAAATGTGACGACCCCAAAACACAGAGACCCCG[GA]TGAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177 G A TAGTC	TTTTCTCCCTT CTTAAAGAGA		AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACTTAAGGGTTTAGCAAAATTCACCTGACAAAGAGTAGGTTTACACATTGACCTCATAAAGTGATTTTCTCTTTCTGTGTTTCTCCCTCTTAAAGAGATAGTC[GA]CCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37 T A TAGATTC	AAATTCAACC ACAGATCTAT		TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAAATTCACACACAGATCTATTAGATTCT[TA]CACCATCTCAAACATATCACATCAAAGAAGCAAGGAGACATATTACTGGTGAGGAAGGCCAAATTCAA
WI-3208	140 G A AGATAAAGA	GTGGAGTGGGC		TCACTCAAAC AGGCTTGG	CAAGCACACATTACAGGAGTGGGAGGTAGGGAAGGTGGGCAACTTCCGACGACAGAGAGGGAAGAAAGTCAGACCGTTGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGAGTGGGCAGATAAAGA[GA]CCAAAGCCCTAGTTTGGTGGACACTGTGGGGATTCAAG
WI-1775	47 C T TTTTCTCTG	CCTGCATGGTC		AGTTGAGATT ATGACAAATGAT GTAAA	ACTCCACCAACAGTTTGTGAGCCAAACCCGTCATGGTCTTTTCTCTG[CT]TTTACATCATTTGTCATAAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A ACAT	AGCATATTCA TTGATTTCTCT		GAGGACTTAAA AAGGAGCATTT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCATTGATTTTCTTACAT[GA]CAAATGCTCCTTTTAAGTCTCAACTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCTCTTAGGA

WI-3416	33	C T	CCAAGTTGTA GCATTCAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCGTGTTCTCTCCAAAGTTGTAGCATTTCAGAAAGTC/CTCTTAGAGGTAGTTGTCTCGTCTGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACCTCTCTCCAAACAAAGTGTACCAACAGCATTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGCGACACATAATTAATCCCATTCCTCTAAAGAGCCAGG TCCTATTCTTACAAACACAGAAATTTAACAAATTTGAAATCAGCTACTCTCTTAGGCCCATCAGAG AATCT/TAAGATCATGGGAAATTTGATGCCATGTGAATTTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCGACTCCAGAGCCATCATCTGTAAAGAC
WI-3453	70	C T	TTCTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACTTAAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGT/ATGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474b	109	G A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACTTAAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCAC/ATGATTTAATGAGGTGGTGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90	A G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	TTTGACCCCATACATGAGAAATAAACCAATAAGAAATGGTGGAAAAATAAACCGGAGAGACCTGGG TTTCTGGATGTCT/CTTGGAGACAGGGTCACCCAC
WI-3502	79	C T	CCTGGGTTTCT GGATGTCT	GGGTGACCCCTG TCCTCA	TCACGGCAAGTTCTGCAGCAGTGTCTTGAACCTCTGCTGTTTCCAGAGTGTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCT/CTG/ATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3600b	146	G C	CCATGCCCCTG CATCT	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGAACCTCTGCTGTTTCCAGAGTGTGATTATCCATGCCCTG ATAGTTCTGT/CTGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTACAAA
WI-3600a	78	T G	CCATGCCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TAAATCATGCTTATTTTACAAAGTAATCCACTCACAATAGGCAATTTGATGTCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACCTTCTACTTACTGTCTGTTATGATGCACCT/CTCTTTTGG ATAGATGGTTGATAGGAGATGGGTTTAAAGACACAATTTACCTTGTGTTTTCAGGCAGAAATAG ACTCTCTCTGTGTAAATCACTGAATGAGTTCCAAAAGCTTTATGTCTAC
WI-3678	125	G T	---	---	AAAGCGATGTTGAGATACCACATTCATGAAAAAGTAAAAACACACACAAAAATGACATAAAA T/AT/AAAAACTACTATAGTTTATGAAAAATGACTTCCAAAATTCAGAGAAAAAGTCACCTTAAACAGG ATTCTCAATTCATTCAGAAATACTCTCTGTCTTAACTTGACTGCACAG
WI-3687	67	A C	---	---	TCATAAATGTGAAACCAAGAAATCTGACACGACCTAACTGCCAGTCCCTCAGTTATGTATCAATGA AAAAAT/CTACACCGGTTCAATGAAAAACAATGATGGTGAGCCCATGCCCCCTTATTTAATGAAAA GATCTTGGGCAATTAATCTC
WI-3735	72	T C	CCTCAGTTATG TATCAAAATGA AAAC	GGCTCACCAAT CATGTTTTT	TCATAAATGTGAAACCAAGAAATCTGACACGACCTAACTGCCAGTCCCTCAGTTATGTATCAATGA AAAAAT/CTACACCGGTTCAATGAAAAACAATGATGGTGAGCCCATGCCCCCTTATTTAATGAAAA GATCTTGGGCAATTAATCTC

WI-1819	51	C T ---				GAAAAAGCAGGAAGCCAGGACAGGACAAACTTTTGA AAAAGTCTTT CAGCAC[C/T]TTGGTGATCCG AATTTTAGTGTGATTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCCAATTAATGAATGTGGAAAAAAGGGTGGTAACCTGTT AAGCCTGCTGCAATGTTAGACACGAGGGTGGGGTGGGAGGTGAATACC
WI-3746	116	G A ---				GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGTCTCTGC[G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C CAA	ACAGTCATTT AGTCTTCCTGA	TAAGATAACC ATACTAGGTAC ATCCG		AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA[T/C]CGGATGTACCTAGT ATGTTATCTTATCTGACAGACAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C G	TGACCAATGTC TTTGAAGCA	TCGTGGGTGC CTCTCC		CAATGACCAATGTCTTTAGAAAGCAG[A/C]GGAGAGGACACCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACGCCACAAAGGTGAGGAAGCAAGGGTGTCTGGCCACT
WI-3901	114	A G ---				GGACATTGTCCTCAGAAAGTACATTCAAGCCCTGGACGGTGTCTCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCCCTGAACCTCGGCTTCCCTCACCTGACAAAGTG[A/G]TATCATGTGTACACTGC AGTGTATTAAATGCTGCAT
WI-3914	99	C T GC	TGATCTTCTC AAGACTCACA			CTGAGGAGATTGATGCTACTTTACTGAGGAACTTTTATTACCTCCCTGAGTTTGTTCCTTGCCTGCAA GACATTGCTGATTCTTCTCAAGACTCAGACG[C/T]ACCATCCTTCACTTCTCTAGACCTATAACTAG ACTCAAGTCCACAGCAGGCCCTTAAAGGTAAGGTACAAAGTGTGACCCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-4019	33	G A A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA ATG		CCACTCCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTTGTCTCTGTTATTGCTGTTCACAGAGT GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4091	84	A T GTCAATGCATG	TTGAGGTCTTA	TGAGTCCCTAT TAAGTGACAAT ATTGTT		TAATTCACATTGCTCTGTTTGTGCAATTTATTGCTTCTCTTATGTAAACACAAATCACCAACATTGAGG TCTTAGTCATTGCATG[A/T]GTATAACAATATTGTCACCTTAATAGGAACTCAAGCATAGTTATGTT ACATTTATTGCTAACAGCAG
WI-4160	117	A G CAACAGAA	CCATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT AGCC		TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCCTTTTGGGTTAGGTGGCTTCTAAGATGGTAAT ATCTGTCCAAGTTTTTTGTTCTCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A G AAACA	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA		CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGGTGTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT

WI-4177	68 T	TGAATAAGCA CGTATTAAATT C TACCTA	AAGGCAGCAA ATCATGATG	ATGCCTGCGATATACCTTCCAAATGACTAGTATGAATAAGCACGTAATAAATTTACCTATTATATTT AT/C/CATCATGATTTGCTGCTCTTCCAAATTTACTACAAATTTGATTGTACATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4199	51 A	CTCCCCAAGTT AGTCAATATA C AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCACTCCCCAAGTTAGTCAATATAAAAAA[A/C]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAAAACAA
WI-5163	24 C	CTGTCACTGGT CTGCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACTGGTCTGCTGTC[A/C]GGTCTGTTCTCTGTGTTCTTCAATGTTCAACTGCTTGTAT CTGTGCCCACTAAGGTATCAGGTTATATGGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAAATTGCAACATTTGGGCAT
WI-4250b	117 A	---	---	TAAGTGCATTAAGTGTACAAAGTCCACAAATACCTCTTCCACCAGTGTCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACACAGGGGTGGGAAGGATCCTGTAAAGG[A/G]TAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94 G	TCAATATGAG TCITGTGAAAC AGG	CTTTTACAGGA TCCITCCCAC	TAAGTGCATTAAGTGTACAAAGTCCACAAATACCTCTTCCACCAGTGTCTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACAGG[G/T]GTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68 G	TGCTCCCCCAT CACCT	GGCCTACTTCA AGTTGTGTAAG G	TAAATGCTCTGGGAGATAATAGAAAGTCCCATCCCTCTGATACCTTGGTGTCTCCCCCATCACCT TG/C/CCTTACACAACTTGAAGTAGGCCCATCCAAACACTGTGTCAGAAAGTAACTACTGTGAC ACAGCCTCTTCAATGGCACAAATCAAAAGCACCCAGTAAAGAGAGGCAAAATCTGG[C/T]CTCAC CATTTGAAAAGTCTCTGAAGGATAAGGGAGTGAATGACTGCTAGAGAGAAATGATTGGCCTT
WI-4256	57 C	---	---	AGTTCACTGCTAGATGAGTAGACCATTGTCCTTTTAAATGACTCTTCTTGGTCTCTCAAGATATCACCAGCCAC GATG[C/T]TACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4325b	71 C	---	---	AGTTCACTGCTAGATGAGTAGACCATTGTCCTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCAGCCAC CCAGGACACTGCCATATCT
WI-4325a	58 C	---	---	TGGGCAGAAAGTCGGGTATGGCAAGTCAGGGTGGTTAACTTGGATGCCACTTCTGCTGTACCTTCT CTAGACTCTTGACCTGCAGGAGGATCCCTGGCCTCTGAGTTTATCATCTCCCACTCCAGCCAG GGCCTGTATCTGTTGAGGGCC[A/G]GAATCGTCACGGCTCACAACTGTGGAGGTAGGAATGACGA G
WI-4347	158 A	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGGCAAGTCTGCTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACAGTGGGACACAGGGGTACTTGTATCACCT[C/C]TCCCGCAACCCCA AGCAGCACAGCTTGACGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAAGGAGAGGGGAAGAGA AAAGAGGACTTTGACACACAACTTGA
WI-1936	117 T	---	---	AAAGAGGACTTTGACACACAACTTGA



WI-5204	54	C T ...			...	TAGATTTTATTGATGACAATAGGGAAGCCCTTTGTTAAATGGGTTTGAAGAA[C/T]GAAGAAAAA TGAAAAGGGAAGAAATTGACAGAAACCAGAGAGTGTGAGGGGACGCAAAATCCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70	A G C T C A A A A A	GGACCTTAAT ATTTAACAGA TTCCG	AGATAATTTTG TAAAGATAGTT TTCCG	AGATAATTTTG TAAAGATAGTT TTCCG	TTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[G/G]GCGAAAACATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCCT GTAGTCAAGGTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112	T G A T A T A A	TTGTATCAAA GAGATGGGT GATATAA	AATTAAGAA ATCTTTACATG GTTCTT	AATTAAGAA ATCTTTACATG GTTCTT	CCCTGAATGTGCTTTGCTTCTCTCCCACTCTAGGAACTTTTCCATGTCAGGTGAAGGTTTTGA AGAGTCTTTAATTAACCTGTATCAAGAGAGATGGGTATATAA[T/G]AAAGAACCATGTAAAGATTT CTTAATTAGTGAATTCATCAGGGCTCTCCACTGCTATCAGTAA
WI-4456	49	C T T A G T T C C	AGTTGAATTA TTCAGAAAAT TATAGTTCC	TTTCTGTTAT GCATGAACCTTG	TTTCTGTTAT GCATGAACCTTG	ACACATTTTCATTTGCTTTAAGTTGAATTTATTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAGGTGGGCAATTGATTGAATTGT
WI-4461	49	A G C C T T C C	TCAGTGTATT TTAAAATTAT G C C T T C C	TTTGACCTTTG ACCAATTTCA	TTTGACCTTTG ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAAATTATCCTTC[C/G]TGAAATTTGGTGAAA GGTCAAGAAATGAAATTCACATTTTAGATTTCTGGAAATTTTATTTGCGATGATAATGCAATGGGC
WI-4465b	75	G A ...		...	...	CTACTGGATTTTACTTTGCTCAAGCCAGACACACAGTATATAAGAAAAACAGTTAGTAATCTT TCACCTTT[G/A]TATTTCTCTCTACCTCAGGGAATC
WI-4465a	41	A G A C A C G A A A G T	AAGCCAGACA ACACGAAAGT	GGTGAAGATT ACTAAGTGT TCTTT	GGTGAAGATT ACTAAGTGT TCTTT	CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGT[G/G]TATAAGAAAAACAGTTAGTAAT CTTTCACCTTTGATTTCTCTCTACCTCAGGGAATC
WI-1949b	160	T C T A A T C	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAAA	TGAGAGGTGGG GACAAAAA	GGGGTTAGGACCTCGAGATCTTTTCAGAAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGCTGAATATATGTTGAAGAAATAAA GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCCACCTCTCACACCTTTCCCTGG CACA
WI-1949a	86	T G A T G C T G A G T	CAGTGTGAG ATGCTCTGAGT	CCATGTCAGCA GCTTGG	CCATGTCAGCA GCTTGG	GGGGTTAGGACCTCGAGATCTTTTCAGAAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/G]CAAGGCTGCTGACATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCCACCTCTCACACCTTTCCCTGG CACA
WI-4529	64	T C A A G A T G	CCAAGTAAGT CTATCATTCTG	TTCTAAAAATA ACACTTCTCTGA AAAA	TTCTAAAAATA ACACTTCTCTGA AAAA	TGAGAGAGTTTTGGATTATTCATCTCTGCAACACTCCAAGTAAGTCTATCATCTGAAGATG[T/C] GAGTCTCTTTTATATCTCTATGATTATTTTTCAGGAAGTGTTATTTTGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGGTGCTGGACAAGATGGGCCCTAGGATCATTTT

[illegible]



WI-2038	155	C T	TGTCCTTAAA GTGTGAAGT ATTAATTAG	ATTCTCTTG AAAGAAACAT CA	TCAGGTGACAGAAAAAGTCACATTTCTCAATCACTCACTGCTGTTATTTGCTCTTGCAAGTGT ATCCAAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAAAAGTGTCTTTAAAGTGTGAAGTATTA ATTAGATTCTATTTTATGATA[C/T]TGATGTTTCTTCAAGAGGAAATTTGTGTAAGAGGATTCCCATTT TGCAATTCATTGGC
WI-4782	113	C T	GATGCAGAAG ATAACTAGAA AATGC	GAACCTCTTG GTTATTTTCT GTTC	TCATTGACTTTTAGAGTTCCTTCAGTCTTTATGCTTATTTCTTTAGGAAAAAAGTAGGCTAGGAGAA CACAAATTCAGGTTCTCTCCAGATGCAGAGATAACTAGAAAAATGC[C/T]GAACAGAAAAAATAACCA GAAGAGTTCATTATGGTTTCTCCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAAATCAGTGCATAGAATCATCTTGCTAAGTTC[AG TTGAAAAAAATTAATGCCAAAATTTAAATTTATCCAAAATTTAAGTCGAGATTATAATTGATAATTT AAAAACTATATTGAGTCTTTCTAAAAGATGGCGTATCACTCTA
WI-5300	38	T C	TCCAGAGAC CACTTCATTG	CTACTCTTCT ATTCATAATC CAAAAA	CTTACTTCCAAAGTGTTTCCAGAGACCCTTCACTTCTT[C/T]TTTGGATTATGAATAGAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAATGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAGTGCAGAGGCCA
WI-4818b	121	G T	TGATAATGGG GOCCTGTT	CCITCCTTTTA TATGATGCCA GA	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAATTTATCAAGAAGGAAAAATATACATATGGGGTGATAATGGGGCCCTGT[G/T]CTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	A G C	TTGCCATAGAC TAGGTTATGTC	CATATGTATAT TTTCTTCTTG AATAAAT	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCC[AG/C]CACATGAATAAACAATCTTAT ATAATAATTTATCAAGAAGGAAAAATATACATATGGGGTGATAATGGGGCCCTGTGCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	T C	TTCCATTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTTGTGTTGATTTCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAAATAATGATGTTATATATATACAAATTTCAACTCAACAGGAATCCATTTCTGGTAGCAGGT ATA[T/C]GGACTCATTTCTTCTTTCATCTATTTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G A	GCAAGATATA AAGATTAAAG AAAGATAACA	CAATTCCACTA CCTCATTTATT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATGCTTGATAACTGGAGTAGTGCCCTT
WI-5328	44	A G	---	---	AACATTTTTAACCATGCTACATTTACAACACTGAAAGACAG[G/A]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACTGGAAAGAG
WI-4897	93	A G	---	---	GCCTTTTGGAGTTTAAAGTCTTTTGGAGTGTCTTTTTCCTCCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAAAATAAGCGCTTGG[AG/G]GATAAACACATCTTC
WI-5345	29	G A	---	---	CCCTGCTATAGGTCAGTTTAAAAATCC[G/A]CCTGCTATGGTTGCTTGTGAAGCCACATCCACT GAGGTATATTCTGCTGCATTTTCTATATCACTCAGCTTCAGATCCACTCCATCAACTTGCAG

WI-5370	143	T C A T A A A A C A A	A A T A A G A T G G T A C C T T A A C T A	C A A A G T T G G T A C A G A G A A T T T C A A A	T G C A T G T A C T T C T T G G A A T C A T A A A G G G A T C T G A G A G C C T A C A G T A T A T G G C A A C A T T A A C C A A T C T T T T G A A A A T T A C C T G T A T C C C A T C A T G G T T C A T T T G C A A A A A A T A A G A T G G T A C C T T A A C T A A T A A A C A A T T C T T G A A A T T C T G T A C C A A C T T T G C T T T T C
WI-9711b	423	T A		---	G A T C C C T T C A T C C C T C T C C A G A G A G G A G A G A G A A C A C A A G A A A A C G C C T G G T G C A G A G C C C C A A T T C C T A C T T C A T G G A T G T G A A T G C C C A G G T G A G G A G A C G G C T T G C T G T A G T G G G A A A G C A C T G G A C C T C A A C A G T T G G A A A T G T T G A G T A G T C G T A T C C T T G A A G C T G T G C A G C A G C T T C A G T T C T T G C C T G T G G A A A T A T T T C C C T G A T A C T C T T A A A A T T T G A A T G
WI-9711a	390	C A	---	---	G A T C C C T T C A T C C C T C T C C A G A G A G A G A G A G A A C A C A A G A A A A C G C C T G G T G C A G A G C C C C A A T T C C T A C T T C A T G G A T G T G A A T G C C C A G G T G A G G A G A C G G C T T G C T G A T G G G G A A A G C A C T G G A C C T C A A C A G T T G G A A A T G T T G A G T A G T T A G C T G T C G T A T C C T T G A A G C T G T G C A G C A G C T T C A G T T C T T C G C C T G T G G A A A T A T T T C C C T G A T A C T C T T A A A A T T T G A A T G
WI-9702c	345	G A	---	---	G G A G A A T T T C A G G G T G A T G G A C T G C T C C C G C T C T G A T T C A C T G C T A C T A G C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T T A T T C T A A C T T T A A T G A T C T C T G T G A C T T T T A T A C T A G C T T T A A G A G G T T T C A T T C C A G T G C T A C A G C A T C T G A T A G
WI-9702b	344	C T	---	---	G G A G A A T T T C A G G G T G A T G G A C T G C T C C C G C T C C T G A T T C A C T G C T A C T A G C C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T T A T T C T A A C T T T A A T G A T C T C T G T G A T T A T A C T A G C T T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C T G A T A G
WI-9702a	179	C T	---	---	G G A G A A T T T C A G G G T G A T G G A C T G C T C C C G C T C C T G A T T C A C T G C T A C T A G C C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T T A T T C T A A C T T T A A T G A T C T C T G T G A C T T T A T A C T A G C T T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C T G
TGR- A003N21	49	C A	---	---	T A T A G T A T T A A C G A A G C C T A G A A G C A G G C T G T G G G T G G T A T T G G T C A J A G C A T A T C T A G G T A T A T A A T A A C T T T G A A G C C A T A A C T T T A A C T G G A G T G G T T G A T T C T T T T T A A T T T A T T G G G A G G G T T G G A T T T A A C T T T T A A T G T T G T T A A T A T A A G T T T T G T A A A A G G A A A A C C A T C T C T G
TGR- A004V30	203	C T	---	---	T G A T T A C C T C T C A A T C T A T T T G T A G A A T G G C T A C T T C A T A G G C A G A G C A G C C A C T T T T G G C T A A T T T T A A C A T C C A A A G C T A A T A A A T A A T C A A G A A G A A A T A G A G A C A T T A A C A A A A T A A A T T A T G T C T A T T T G G G A A T A C C T A A T A T C A G A T A C T A A C A A G T A C A G T G A T A A G A A T A A A A A G A T A A T A A T C A C A C A T A C C T T C T A G G T T A G T A G A A A A G C G G, T T C T C T A G G T T A G T A G A A A A G T T

TIGR- A004W22	232 C A ---	---	GGATAATCAGTACAATAATGGGGACCTTAAACTGCTGTGATGCAGGAGTGGAGGGCTGGGCAGTG CCGAGGCAGGGAGGAGGACAGTGGGACCAAGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGCATGGGAATGACCAGGTTCCACATCATGCACAGCGGGCCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTTGGTGTGCCCCCGCCTA[C/A]CTGGAGATGCTCTAAAA
TIGR- A005D24 b	138 C T ---	---	CATAGAAAGGAGCTTTGAGTATTGACAGTTTGAAATTCCTTTGAGATAATTGATTTTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCCAACATCTTTATAGAGAAATAAAACCCCAATTT CTC/TJTTCAACCATTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACCTTTATAAATTAAGGAAACAAT
TIGR- A005D24 a	123 A G ---	---	CATAGAAAGGAGCTTTGAGTATTGACAGTTTGAAATTCCTTTGAGATAATTGATTTTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCCAACATCTTTATAGAGAAATAAAACCCCA TTTCTCTTCAACCATTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACCTTTATAAATTAAGGAAACAAT
U03735	74 C G ---	---	TGAGTCTGAGCACGAGTTCAGCCAGGGCCAGTGGGGGCTGGGCCAGTGCACCTTCGGGGGOC GCATCC[C/G]TTAGTTTCCACTGCTGTCGCTGACGTGAGGCCCATCTTCTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTCTCTGTTGA GTTGTTCAAAATGTTCTTTTAA
U39840b	42 T C ---	---	GGTTTGTCTGGCATAGCCATGCTGGTAGAGAGAGAAAAAT[C]CAACAGCAAAACCAACCA CAAAACCAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTTCATTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGTTATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
U39840	56 A C ---	---	GGTTTGTCTGGCATAGCCATGCTGGTAGAGAGAGAAAAATCAACAGCAAAACCA[A/C]JACCACA CAAAACCAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTTCATTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGTTATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
WI-8997	41 G A OCCC	GGCCACTTGCT AGTGCTCA	GTGGCCATCGATCTGACCGTCCCTGCCACTTGCTCCCC[G/A]TGAGCACTGCGTACAAACATCCA AAAGTTCAACAACACACCAAGAACTGTGTCTCATGGT
WI-7008	180 A G ---	---	TATACCACTTCCATTTGATGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGTCAGAA AGCAACCAAGTTGATGATAGGAGTTCAAGTCAATATGGTCACTTGATGACCCAGAGTCAAAACATTTCAG TTTCCACCAAGCCAGTAACAGGCCAAGAGCTGCTCTCAAAAG[A/G]AGAGTAGTTATCTGCAGA AGATGGCAGGGCCTTGCTCCGAAAGCCTAGAGACCGCCACTGTGATTACCT
WI-9005	26 C T GGGAACTCT	CGAATTTGCTG AAA	GGTCCCACGAATTTGCTGGGAATCT[C/T]GTTTTTCTTAAAGACTTTTGGGACATGGTTTGACTCC CGAACATCACCGAGCGTCTCTGTTTTCTGGTGG

WI-7593	46 G A ---	---	TTTTGTTGCTCTGGACACCCTGCTCCAGGATGAAGGAGAG/GAATGAGATCAGTTTGGACATTCCTCTTGAATATAAGAAATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCTCCAAAGTGCATCTTGGGGAAAGGCTCCAGTGTATCTGGACCAGTTCCTTCATTTTCAGGTGGGACTCTTGATCCAGAGA/GGACAAAGCTCCTCAGTGAGCTGGTGATATATCCAAAGACAGAACCCCAAGTCTCCTGACTCCTGGCTTCTATGCCCTCTATCCTATCATAGATAACATCTCCACAGCCTCAGTTCATTCACCTATTCTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTAGATAAGA
WI-6962	78 A G ---	---	GCAGAGAAGAGAACCATGCCAGGGGAGAGGCCACCGCATC/GGTGACCCAGCGGAGGCCAACTATCCCAAATATACCTGGGTGAAATATACCAAATTTCTGCATCTCCAGAGGAAATAAGAAATAAAGATGATTTGCACTCTTAAAAAA
WI-7059	43 C G GGCATC	AAGGCACCCA GGTCA	AGCAGCCATCACATGATCTGTTTTTACCACITTCACCTGAAAGACACCATTTAT/C/TTACCCCAAGGCGAGAAAGTAGAACTTACTATTCAATAATGTTGACACAATTGGAATTGTC
WI-9063	53 A C TT	CACTTCACTGA AAGACACCAT	AAGGGCATTGAGACTATAAGCGAGTAGACAATCCCAACATACCATCTGTAGAGTTGGAACCTGCATTCTTTAAAGTTTTATGCATATATTTAGGGCTGCTAGACTTACTTCTCTATTTCTTTCCATTGCTTATCTTGAGCACAAATGATAATCAATTTATACATTTATACATCACTTTTGGACITTTTCCAAGCCC
WI-7079	293 T G ---	---	TTTTACAGCTTGGCATTTCTCGCCTAGGCCTGTGAGGTAAGTGGAT
WI-9074	38 A G AAAAG	GGTAAAAGTT CTTTTGTCT	TGGATGCCGAGGTAAAAGTTCTTTTGTCTAAAGAA/GAAGGAACTAGGTCAAAAATCTGTCCGTGACCTATCAGTTAATAATTTTAAGGATGTTGCCACTGGCAATGTAACGTG
WI-7104b	249 C T ---	---	GGAGTTTGGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGTTGGCTTGACCAGTCACGTTGGGAAGAGAGAGAGTGGCAGGAGACCCCTGAGGCGAGCCGTTCTTCTGACTGAGAGAAGGGAGGCCAGGGCTGGAGCAGCATGAGGCCACAGCAAGAGGCTTGGTCTGAGGAAGCAGATGTTTCATGCTGTAGGCCCTTGACCCAGGTGGGGGCCACAGCACCCAGCAGCATCTTGTG/T
WI-7104	157 C A ---	---	GGAGTTTGGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGTTGGCTTGACCAGTCACGTTGGGAAGAGAGAGAGTGGCAGGAGACCCCTGAGGCGAGCCGTTCTTCTGACTGAGAGAAGGGAGGCCCCAGGCTGGAGCAGCATGAGGC/C/AGCAAGAAAGGGCTTGGTCTGAGGAAGCAGATGTTTCATGCTGTGAGGCCCTTGACCCAGGTGGGGGCCACAGCACCCAGCAGCATCTTGTGCT
WI-8974	34 C T AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAAATGAGAGCCCTGAGCCCTCAAGAACTCA/C/TGCCAGCTCAGCCCTACACCAGTTTCCACC
WI-9161	61 C T CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	TGGAGTTTCATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
WI-9014c	93 T C ---	---	CTGTGAGGGTGACGTTAGCATTACCCCAACCTCATTTTAGTTGCCTAAGCATGGCTGGC/C/TTTCCTGTCTAGTCTCTCTGTAAGCCAAAGAAATGAACATTCCA
			CCCTGTTCCCATGCTGACCTGTGTTTCCCTCCAGTCATCTTCTCTGTTCCAGAGAGGTGGGGCTGGAT
			GTCTCCATCTCTGTCTCAACTTTAT/C/GTGCACTGAGCTGCAACTCT

WI-9014b	44 C T ---	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCTCCCAAGTCATCTTC/TGTTCCAGAGAGGTGGGCTG GATGCTCCATCTGCTCAACTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGAGACCCCTGGTGCT CAGTGCCCTTTAAGTGCAATCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTACGGGTCCCC TCTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/A/CACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGAG/C/CCCTGGGT GCTCAGTGCCCTTTAAGTGCAATCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTACGGGTG CCCTCTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	---	CTGAAATCCCTCTCTGCCCTGGCTGGATCCGGGACCCCTTGCCTTCCCT/C/TTGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCGACCTCTCTGGCCCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAGTTGTGAAGCAGAGAGAGAAAGCTGGAGAGCCGTGGGCCAAT GGGAGAGCTCTTGTTATTATTAATATTGTGGCGCTGTGTGTGTGTTA
WI-9171	62 G A ---	---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAGAAAGTAGAGATAATAATCA/G/A/ TTCTTTACAACCGATGGTAATTAAGCTTGATTCAACAAGACTTCATGC
WI-9174	47 T C T	CTAGACCCC ATTCTCCTATT ACTG	TCTAGAGGTA TATAGGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATCTCCTATTAT/C/CAGTCTGTCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAITGAG
WI-7753	52 A G	CCATGTTCCGA GAAGAACAGA A	CAGAGGCTTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCGAGAGAAACAGAT/G/ATCCCTGTATT TCAAGACCTCTGTGCACTTATTATGAACCTGCCCTGCTCCACAGAAACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAATCCATCCTGCTAAGTTAATGTGGGTAGAA
WI-9186	76 G A	CCACTTCTCCC CGCA	AAAGGGAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAACAAAAAATGGCATCACCTGTCAAAAAATGGAGTTCCACT TCTCCCGCA/G/A/ACCTAGGTACAGACTTCCCTTTCATCTT
WI-9193	94 G A CA	AGAATATTGT CTGCCTTAAAG CA	GGTGTGTGG TAGGGG	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGATAA CTCAGAAATATTGCTGCTGCTTAAAGCA/G/ATACCCCTACCACACACACCCCTGTCTC
WI-9015	48 C T ---	---	---	TTTGATTGATATCGTGAAATCCTCAGCCGAGAAATGGGTGGATTG/C/TTGGTTAATACAT CTTCCCTAAAGAAGATAAACACAAAAATCCATTCCAGGTAGCTCGGCCCACTAAAGAA
WI-7254	37 A G	GGTCTGAGAG AGGAGCCAC	GGAGTGGGTGT CATTAGGA	GGAGCCAGGAGACAGAGGCTGTGAGAGGAGGCCAC/G/ATGCCCTAATGACACCCACTCCTAGCC CTGAGGCTCGTGGCCCTCAGACTGGGGAAGAGTCCAGGAAGGGAGGAGGCCAGCCACTCCTCAATGC TCAATGGTCCCCCTGAAATCAAGACAGG



WI-9231	32 G	CAGTCCCCA GATTGA	CACTGCCCCA ACTCAGAC	GTGACCCGTGAGGTCCGCCAGATTGA[C/C]CTGAGTGGGCAAGTGTGTCAAAAGGGGCG TGCCCCCAGGAGATAGGCTGAGAGCAGGGAGTTGAGCCGAGAAGTCA
WI-7836	120 T C	CAAATAAACA ATGCAACGTTG	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTAGTAGTTACTGAAAGAAAAGTCTGCTA GAATGATAAATGTCATGGTGGTCTATACTCCAAATAAACAAATGCAACGTTCC[C/C]GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCCAGCT
WI-7286	65 T C A	CAGCTTCAGCT TAAGTGACAG	AAACAATCTA ACCAGAAAGCT TTAA	TCCATCCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTAAGTACAGAGAT[C/C] TGTTAAAGCTTTCTGGTAGATTGTTTTCATCTGGTGATCATGCTTTTCCATGTGTACCTGTAAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT ACGTGAATTTT	CCCAATTTTA TTAAAAGTTTA CATCTAT	CAAAATCTTGGAAATATCTCAAATGTTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAATTTGTTATAGATGTAACCTTTTAATAAAATTTGGGTGTGG GAAGATTAAAGGAGGGTGTCTCTGTGGTCTCCTCCCTGCCCTCTCCCA[C/A]GTGGGAGAGACC TGTGATTTGCCAAGTCCCTGGACCTGGACCAAGTACTGGGCTTATGGTGGGGTGTAGGCAGG TGAGCGTAAGTGGGAGGGAATGGGTAAGAACTACTCCAAACCTAGGTCTCTATGTAGACACCAG ACCTAGGTGCTCTCTAGGAGGGAACAGGGAGACCTGGGGTCTGTGGAT
WI-7860	50 C G	CGTACCTCCAA ACATAATTGA	GCTTGAGTGA AGTCTGCAGA	CAAGGCGTACCTCCAAACATAATTGATT[C/A]GTATCTCGAGACTTACACTCAAGCAATCCTGAGG AATCTGAGGAGGGCTGGCTACTGTCTCTGCACCTGTGCTGTTG
WI-9064	29 A G TTC			CACACTGTCTGTTCTTCACTGTCTGAGGTCTGGCAGGGTCAGGCTGGGGTAAGCCGGGTTCCACA GGGCCAGCCCTGGCAGGGGTCTGGCCCCCAGGTAGGGGAGAGCAGTCCCTCCCTCAG[G/TA]ACT GGAGGAGGGGACTCCAGGAATGGGGAATGTGACACACCACCTCCGAAAGCCAGCTTGCACTCCAGT TTGCACAGGGATTGTCTGGGGCTGAGGGCCCTGTCCCAACCCCGCCC
WI-7307	128 G T			GAGGAAATGTGACTTTCACTTTGGTG[C/T]CAATGGACAGAAAATCTACCTGTGCTACATAGGAGAA GTTTGGAAATGCACCTAATAGCTGGTTTACACCTTGATTTCGAGGTGGAAA
WI-9274	25 C T G	GAAATGTGAC TTCACCTTGGT	CAGGTAGAATT TTCGTGCCATT G	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTCTTAAAT TGTTTGCAGTCTTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTTTTGTTTATGTTTAAAGTAACCTATTATCTCTGGAATTCATG AAGGTGAATATCGTTTTTGTAACTGAATAGAATTGTATAGCGATGA
WI-7313e	266 T C			AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTCTTAAAT TGTTTGCAGTCTTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTTTTGTTTATGTTTAAAGTAACCTATTATCTCTGGAATTCATG AAGGTGAATATCGTTTTTGTAACTGAATAGAATTGTATAGCGATGA
WI-7313c	256 C T			



WI-7424	131	T A	CAAGAGAGAG AGAGGAAAGA AAAA	TGCAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGGGAAGAGCAGAAAGTTAGAGAAAAAAGCCACCGGAGGAAAGG AAAAAACATCGGCCAACCTAGAAACGTTTTTCATTCTGTCATTCCAAAGAGAGAGAGGAAAGAAAA TT/AJACAACTTTCATTCTTCTTGACGCTTCATAAACAATTCACATA TCCTGCAAGAAAGTTCTCAAGCCTTTTTTGATTTTTTGCAATAAAGTACAGCTTTCATAGAGTGA TTGGGTAGCTTAAATGGATCCATAAACTTCTCTAAATTTAAGTGAGA/CJCTCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAACTAAAAATATGTACCACCTCGTTTATTTGTTTCATTCATCCA TCCCTTTTCCCATGAATATTCA GTGGCCACTACATGTTATAGAAACCATCATCTTGTCCACACGACAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGGAAAAAGCATTAAAAAGTGTCCTCAATTAAGGGGACTTTTAAATCAACCTAA TAACTCTAAATTCGCTGACTTTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAAGGGTCA ATTAATCTTTGATCTTTTTTACTCACTGTTAACTTATATAAT/AJITCAGAAC TACAAATGAATTGCTTTTATTCGGTATGCATCCACATTTTCAGCATTTAGTGCTCTGAACAGCAAG TGGAAAGCAGCAGCAATTTGCCAGGAGGTCAAGCCCAACCAATTCGGGGATCTGCTGTGCACACCGG GTTCTTCTTAATCCCTGCTGAGGATCTTG/GA/GAAGCAGCAGCAGCACCACCAAAACCAAGGCATGCA COGGATTCAAGGTTCTTTTGTTCCAGTTGTCAGATTCCAAACTAGACCCCA AACAGTCAACCAACACATGACAACTGCCAGGAGGCTTGCTTCCCTCCCTTTGCGTCCC ATGTCCATAGTCAAGAGGTGCGGGAGGCACCGATGTAGCTTGCCCAAGGGAGTATTACAGAGA GAGGCTTGGGAA/GC/GGAAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTGCTTTCAAGTAACTGGTATGCTGAA ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTTGATTG/G/GGGCTTCTCGAAAGAAACCTTGCG TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCACA GAATATTTGGGCAGAACCTTGGAACTGGCCACGAGGACATCCCAATATCCCTCCTCCTCAGGG CTCACCCGACATCCTCAGCCAAATGAAGGCTCTGAA GGGTGAGACGGGTTTATTGTGCACATTTACACAGCTCAGCGTCTGGCTGGCAGCGGCATGCTC CTGTGGTGGGCTGCTCTACAAGGGGCTTCACTTTCTCAACCACTATGTACAGTCACTGCTCCAA GGTATGGGCTACAGTCTGATCAGTGAAGTCTGTACACACATTTTACATAAATTACACAGGACTC ATACATGAAAAAT/AJAGAGCCTAAGGGCTGTATTTTAAATGAGAAAAA AACTTTTACAAAATAGGCTTTGCAAACTTCATTACTGAATTTGTAAGTCAATGACTGTGTTGTTTT TAAATATGTACCAAGGAAATACAAATTTGGATATGATCATTTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATCTGCACAGGTGCAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTTCACAG TG/AGCATCTTCTCACCTTAAGTGCAGCTGTGCAAGATGCTCAGTGIG
X86400	118	A C	---	---	
WI-8053	242	T A	---	---	
WI-6190	165	G A	---	---	
WI-6275	148	G C	---	---	
WI-6421	41	G T	---	---	
WI-6905	215	T A	---	---	
WI-9420	202	G A	---	---	

WI-9448	184	G A ---				TGGGGCTGCTTTTAGACTTCATTTCTAGAGCAGAGCACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGCTTGTGGTTCCAAGGCTGAGAGCTGGCACAC(G/A)CACTGGTTTCTAAA TCTCTGGCTGGATTTATCCAAGGCGCATGTTCTTAACGTGCCCGTGAGCAG
WI-9470	204	G A ---				ATGTCAGAAAGAGACACAGACAAGGAGTTTTCCCTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAATCAGATTCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCGAGATTCCTACTAGAGCCGCTGGGGACACTGATGAC AA(G/A)GCAATCAACTCATCTCCTCAAGCTCAGGAGGCTCACCCTCCCAAG
WI-1245b	201	G T ---				GATGATTTCTGAAGTCTCAGCAGCCCTGATTTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGATGATGCTGAGCCATGCTGGCATCACAGGGTGGT TTATTATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC(G/ T)CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---				GATGATTTCTGAAGTCTCAGCAGCCCTGATTTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGATGATGCTGAGCCATGCTGGCATCACAGGGTGGT GGTTATTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---				TTCAAGTATAAGGACAGGCTAGAACAAAGGTTCCCAACCCCTGGCAACCAATGACAGTTTGGACCAA TAACCTCTTGTTCAGGGGACTGCTACACATTGTGGGATGTTTAGCAGCCTCCGTGGCTTACCCCA CTAGATGCCAGCA(G/A)CACAAACACCCCTCCCAACAATCATGACAATGAAAATGTCCTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCTGATTGAGAACCACCTGGTT
WI-5385	110	G A ---				AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCCAATGGTGGGATTGGAAGAGG GAAGTCTCGATAATTTTAAACATATGGTTCTTCCAGGAATCG(G/A)CAATGCTAATCTATTGCTTAA TCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCTTGAC CCCTGCTACGGGAACATTGAATGCA
WI-5403	199	T G ---				ACCAAACCGTTGGCAAAAGGCTCCCCAAGACTCACCACCCCACTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATATAATATAATTGCTACAATTTTCCAGTAGTTACCAGGCACCCAGCCTAT TGGAAGAAATCATAAATGTAACCCCTACAATGTATTGCTCTCTGGCTGGTCCAGGCATAGAGTT/G JGGCCTACAACCCATTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A ---				TGATATTTTCCCTTCTAAATGTTATGATTAATAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAATAAGATATAGTTGAAACCTCTAACAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA(G/A)JAGGGAATGAGAAAAAGCACCAACCAGAAAAAAGTGTGT GGCTTAAGGGGAAGCCCAAGGAAGTTAAGT

WI-5801a	48 A G ---			TGGTATTTTCCCTTTCTCTAAATGTTATGATTAAATAGTGTCTTTGTGAGAAATTTGAAAAAATGT AAATCAGAGAACAGAAAAATAAGTATAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAGTTAAGT
WI-5896	61 C A ---			TTCTATTTAAATCCTGTGCCCATTTGCAAGACTGCATTCAGTCTGCATGAGCCTTAGTTTCICAJTAA AAGCCCCCTCACACCGAGGACAATGTTCAAACTAAATGACTGCAAGTGAGCAATTCCTGTATTA TACAACTGGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAGTTTATTTAACTT
WI-7461	153 C T ---			TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATCTAACGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACITTAGGCTGCACATTCCTG TGGCAGGAGCTGTGCTC/TGTTCCCTGTGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A ---			AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTGGTACTTCTCTTTCTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGATGTTTTCAGATGTGACTTCTACATTTCTGAAACTAGATGAGTTAGGCTCTCTCATCT CAATTGAAAATTCCTAGAA/GA/JAAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49 C T ---			TTTTCGTTAAGTCTTGTGAAGCCACACAGAGTGATCTACTCTCTTACIC/JAAGTGTACTTTGCA TATATTTATGGGATGATCTATCCCTACTTAAGATTTCTCTCTCAGGTTAAATATCCATTCTCT TTGTCAGGAGTTCTTATTTGGCCTTCTTTCTAAACOCCTAACCATTTCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---			GAAAACTCGTTGGCTCAAAGGAACTGTAG/JCAAATCTTTTTTTTATTTTGTGTTTTTAACTC AAAGAGTGGAGTTTGCATTGACCTTGTGATGGCAGCTGCTCTTTTGTGTTGGTAAATCTCTAGT GGGCACTTTGCAAAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAG TAGCAAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G ---			AAGGCCAGTGGGAAAGCAGACAAAACACTCCAAGATAC/JAGATATAAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTGATGCTGATGAGGCGATGTCAGACAAAGACATTTGGGTCT TGAGGTTGAATAGGAGTTTGTCTGGTGAGTCTTGCCAGTCCCATAGTAGGTGTTCCATAAATAAC AGTGACTAACTGAGGTAGAGTCACAGAAGAAATTTCA
WI-11152	179 C T ---			GATTTCTTGGGACATGCAGAGCAGATACGGCAAGGATCTTTGGGCATTTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGTCTCGCACCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGACAAAGTGGGACAAAAGGCTTGTCA/C/TCTGTCAAGAAACATTGAA AACAGCCAGTACATGCCACTGTATAGA

WI-1968	167	A G ---	---	TGGTGAGGAGCTGTAGGCTGAAAGAATAGTCTCTGCTCTGGTCTTTCGTTGGAAATGGATGAGTCCTTTACAAAATTTTCCCTTGGCATGGGTGTTATGTTAGAAATCATGGAGTTGGAAAGACTTAGATTCAATTTGGGGCTGTACAGTTTACTGGAAGTTGTTAGJTGAACTTGAGCAAGTGTCTCTTAATGTCTCTCA
				GCCTCAATGCCCTTCCCTGTAA
				GGGTTCAATTAACAGGCTTCCACTGGGTCTCAGATTGCACGGAGATGTAATAATAGGAAGAGATAGAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACACACATTAAACTCTCCCACTCTATA
WI-4701	198	G A ---	---	CCCGCCAAAGTCTACCTTTTGGTCTTTTATTTCTGCTAATGACCATACTATTCCCAATTAGA[G/A]CCATGTCAATTTTCAGAAAAGCAGTATA
				TTATCTTTCCAAACCATGTGTGTTTCTTCACATACCTTTACGTAATTTTAAATCATGTCAATTTAAATTA
				TGCACTTACTTGGTACCAGACATGCTTCCAAATTTGTAATTCCTTAACAACAGCAGCAAGCATAACTGATGTCCATCTTTGTATTCTCTAAAC[C/A]AAAGAAAAGTGTCTTTTGTGTCATCTGCCCTCTCTGTCTTCTCTGTTTCACCTCTGTATTTCCCTATTACGCAATTCATGATTA
WI-4823	164	C A ---	---	AAAAAACAACCTTCAATTTGACATTTAAGAAGATAAAGAAAAACAACGATCCACTGTGTGTTGCTTTGATTTA[G]GGAGATAAAACCTGATCTCTAAGAAAATTAACCCAAAGCAGTACACTAAAAATAGCCTTTGTGTGTGTTTTCAGGAAAGAAAGCCAAATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCACTCTAACTTCCACATAGACATTAAATATAGCA
WI-4860	72	A G ---	---	TGAAGGACCATGTCGAATGCCTACCAAGGTAAAGTAATCGGAGGGGAGGAGGAGTAGGAGTTGCTTCCGGATGTTGCATAAAATCAGGTTCTTTAAGGAGTTCCGGTCC[C/A]AAAAATTTTAACACTGATGCTGTACAAACGCACATAGAAATCGGTGATGATTGCGGTTCTCTAGTAAGTAGCTAATGTTTAGATA
WI-9705	111	C A ---	---	TGATTTGAATTAATTTGCTGTGTTCTTGGTG
				CAATAATCTCTGCTTAGAAGTTGCTTAGGGCCATGGATTATGTAAGGGTGGGCAGGGTGGACTGAAGATCTGTTGGCAGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCATCTTGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA[G]TCCCTCCAATTTTCAGGGGCTCCC
TIGR-A004248	177	A G ---	---	GTGGGATGGTGGAGCCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
				GGGATTCAATGTGTCTGTCTCATCCAAATAGCACATG/GCATGACCTCAGCCCCCATACTCTTTCTTCCCTATGTTCCAGAGACAGATAGACCTGGCCCTTCTCTCTAGGGGATCACAAATTTGGAAGGATGAG
U17579	34	T G ---	---	GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC
				TGGGAGAGGGGATCCTTCTAGTTGA
				GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTTCGTTAACTGTGTATGTACATATATATTTTAAATTTGATTTGAAAGCTGATTACTGTCAATAAACAGCTTCATGCTTTTGTAAAGTTATTTCTGTTGTTTGGGTATCCTGCCAGTGTGTTTGTAAATAAGAGATTTGGAGCACTCTGA
WI-7747b	88	T G ---	---	GTTTACCATTGTAAATAAGTATATAATTTTTTATGTTTGTGTTCTGA

WI-7747a	44 T C ---	---	---	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCTC/JTTCGTTAACTGTGTATAC ATATATATATTTTAAATTTGAATTAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAAGTT ATTTCTTTGTTTGTGTTGGGTATCTGCCAGTGTTGTTGTAATAAGAGATTGGAGCACTCTGA GTTTACCATTGTATAAAGTATATAATTTTATGTTTGTCTGA
WI-7189	197 T C ---	---	---	TCCAGAAATTTCCCTCTCAGCTCATTTTGTCTCTCACAAATTAAGGAGTAGGTTAAGTGAAGGT CACATACCATTAATTTCCCTTCAACAATAATATTTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATTAAGCCTACAACATTTTTC/JAG TTTGCAATAGAACTAATACTGGTGAATAATACCTAAACCTTGGTTATT
WI-7850	57 G A ---	---	---	AGCCCCAGCTGGACTCATGGATGTGCACCCCTTGTCTCCCTGCTCTTCTGCCCTGGG/JACTCATGTA TCTGGCAGCTCTGTTACCCCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCCTGCCCTTGAAGCT GAGAAAGCACAGGGCAAGGAGCAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAAATCAGGGGGCTGTCTACTAGAGCC
WI-7907	69 G C ---	---	---	CTCTTCTTCAATCCCATCACCCCTAAATAGGTGAGGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G/GC/JAGAAGTGAAGGAAGATAGGAAGGATATACCTCTCTGTTATTTTAAAGAAACATTTGTTT GGTGACAGCAATCTCCCTGTCCCTATCACTGTAGAGGCCAATTTTATATCTATAAATATAATAAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAATTAATGTCAAAAGTTTAAAT
WI-7919	242 T C ---	---	---	GAAGGCAGCTGGATCACTTCCCGAGTCCCTGGCAGCGCTTGTGTGGAACACGAGAGCTCCTCCT CAGGGCCCTGGCACTCACCTTCTATTCTGTATGTATTTGGTTAAACACTGTCAAAATAATAGAT GTGCCAGATTTAGATTTCTTACCCTAATCTGTTTAAATTTGTAACCTTTATCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAA/JC/JACAACTTT
WI-7928	101 T G ---	---	---	CTCCCTTCTATGTCTCAGCAGCACGTTGGGGCACACTTGTTCATCTTCTGACCGTTTGTGGGCTA TTCCCTCGCAGTGCAGACATCGTCAAAATTCAT/JG/JACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTAAAACTGAAATTCAACTCTTTATATAGGATTTCTTTT CTATCTCCATCTCCTCATTAATAAATACGTACATTTTCGAGGTAATGGTA
WI-7936	131 T A ---	---	---	TTTTGAGTCAAAAGACTTAAAGGGCCCCAATGAATTAATATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATTTCTTGGAGTTAAATGACATATAGACATACACCCAAACACTTACACCAAACT/AJ ACTGAATGAAGAAAGTATTTGGTAACAGGCCATTTTGGTGGGAATCCAAAGATTGGTCTCCCATATG CAGAAATAGACAAAAAGTATATTAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99 T C ---	---	---	TACACGTTCCAGCCCGTTGCCCACTCATCTGCCGCTTGTCTTGGTGGGGGCAGATTGGGTGG AATGCTTTCCATCTCCAGGAGACTTTTCATG/JC/JAGCCCCAAAGTACAGCCTGGACCAACCCCTGGGTG TGAGCTAGTAAGATTACCTGAGCTGAGCTGAGCCTGAGCCCAATGGGACAGTTACACTTGACAGA CAAAGATGGTGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---	---	---	TTTCTAGGCTGTACAGTCTGATGCATGATTTTATAAAATATTTCACTACTCTTGTAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGTA/GTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGCAGGTTCAATGTGGAATAGTTTAACAGTCAAGGAGCTAACTGGTCAGTATTAATGTGTAGC CTACCAAAATAGCCAGTAGTATCTGAAAATGAAAAATAATGAAGTAT
WI-7416	137 G T ---	---	---	GGCAGGAGATTAGCAACAGGATTCATCTGTTACTTACTTGCCTTTTATCTTTCCCTCTTGCCC CAGTCCCTTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTCTGGCAGTGCT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTTGGCAATGTCATCAG
WI-140	252 C T ---	---	---	ATTTGAAGATTGGAGGGCTTTGCAGAGGAAAATAGATTTCAATTGGATCCCCAACTATAATGACA AGTTTTTAATTAGGTGATCAAGGCTTCTAAAGTGAATGCAAGTTGTACCAAGTAAAGTTTATA TCTCCATTGAGCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTAGTTTAAAAATGTGTCATTTGCTGATTGGCATTCCT[C/
WI-198	218 C T ---	---	---	GAGGTCTTTGAGCAACATGGAAGCCCTACTGCTTCAACCCGAGTTCCCGGATCAAGTGTGGCAAC CATGATGGAACCTCTGCCATGGTTTGTAGTACCTGGACCAAGTAGTCAATCCATCCTGACTTTTAA TTCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTACAGCTA CCTGCTTCCCTT[C/T]GTTTAAACAAGCATAGAATATTTCTGAACAAC
WI-205c	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTAAAGAAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTG[T/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACCTGCATATGCTTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	---	TTTCATGGTCCCAAGACAGATTTAAAGAAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGGCTGACTTTTCAAT GCATGAGTTG[T/C]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACCTGCATATGCTTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	---	GAAGACTGAGTTTCCAGGAGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCACCTGTGTCAGCCCAAGTNCCTTCCAGAGGCTCAGACTACCTCTCCATCTCCCT CTCCCCACAACACACAAATACAGAGATT[G/C]AATTCAGGAGCCAGTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTGGTGTCTTGTCTTCTCAAAATGGAAATGG
WI-276b	25 A G ---	---	---	AGCTTTTGAATCCAAAACCCACATTA/GTCTTGACTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAAATACAGAACACCTCTGTGGCTGCCTGAACGAGAGGATGGGGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCTGCTGAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCTCTCTGCTATCCTGATGACTGGGCAAA



WI-276	25 A ---	---	---	AGCTTTGAAATCCAAAAACACATAG/GCTTGACTCTCTTATCCTCCTCTGTTGTAACTCTATCC CTGAGGCAGAAATACAGAACACCCCTGTGGCTGCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAAGCATCTCTCTGCCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCCTCTCTGCTATCCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	---	TTTCCCAATCCACAGGTAAACTAATAATGGATGATAGAAATTTAGAACTACTTCCG/AJGTTT TTCCCTGGGAAATATTACAAACATTTGGGTGCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCAATTTATGAGCCAGGCTTGTCTGTCAACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAAIT/CJAAATGGTCTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAAIT/CJAAATGGTCTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAAIT/CJAAATGGTCTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	---	GTGTAATTTGGTGGCTTGCACCTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/A/GJTAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATTCTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---	---	---	GTGTAATTTGGTGGCTTGCACCTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/A/GJTAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATTCTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---	---	---	GTGTAATTTGGTGGCTTGCACCTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATTA/GJATGATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATTCTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAT

WI-811	66 GC ---			TTCAAATTAACACCATTGGGTATATTAAATTTNGCTCTATCCATAGTTCTAACCCCTCTTCTCTG/ CJACAGTGAGACACCGCTTCTATTGCTTGCTTGACGTATTAACTGATTCGATCAGTCACCCATCTGGA ACCAAGGTTTCAATTTCTGCTGACCCCTCCCTCCTCACCTACTTGGCTCTGACTTCTTCTTCTGGGCT GAACCTTCTCTGTGTGGCTGTCCGCTTCTCTGCTTGGCTCCAATAC
WI-811b	156 A G ---			TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTATACAGGGGAAGCACTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGACAGCAAGCACAAATCTGTATGGTTT
WI-881	156 A G ---			TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTTATACAGGGGAAGCACTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGACAGCAAGCACAAATCTGTATGGTTT
WI-867b	119 GA ---			AATCTTAACAGCCTTTTGATGOCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCG/AJTTGTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGTTTGAATGTGTCCTCCCAAGCACACATTAGAACTTA
WI-867	113 A G ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCG/AJTTGTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGTTTGAATGTGTCCTCCCAAGCACACATTAGAACTTA
WI-867	119 GA ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCG/AJTTGTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGTTTGAATGTGTCCTCCCAAGCACACATTAGAACTTA
WI-871b	123 C G ---			TCATCAGACCTGAGATTTCAGCATGAAATCTACCAAAGGTACCAAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGACCCACCTACCTCATG/C/GJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACGTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTATTTGTACATAA
WI-871	123 C G ---			TCATCAGACCTGAGATTTCAGCATGAAATCTACCAAAGGTACCAAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGACCCACCTACCTCATG/C/GJAACGTGT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACGTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTATTTGTACATAA

WI-884	198 T C ---	---	AGGTTCTGGACTTGATGCTGGGAAACAATTGGGTNCTGGAGAAATTCCTATTTTGGAGTNTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTTCCTGATCTATTGGGA ACTTCCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCGCGATGCAACATTTATTCAGTGAACAACATGATGAAAATGAACATAAT
WI-921b	205 G A ---	---	CACITCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGACAGTTATACTGG CAGTGATGCCTCTCAGCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-921	205 G A ---	---	CACITCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGACAGTTATACTGG CAGTGATGCCTCTCAGCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-945c	90 G C ---	---	GGCTGGGATGAGAGGTTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTCTAGAACCTAGNAAAGNA GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCTGAGTAATAAGAAA AATCATTAGATAAATGCTCATGACCAAAACAAAGTTCAACACANTAGGTGCAGCACANNNNGGTT TTCTCTGGTCATAGAACTCTTAAAGGGAAATCATGACAGATTTTCTTGGCTTTA
WI-945b	90 G C ---	---	GGCTGGGATGAGAGGTTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTCTAGAACCTAGNAAAGNA GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCTGAGTAATAAGAAA AATCATTAGATAAATGCTCATGACCAAAACAAAGTTCAACACANTAGGTGCAGCACANNNNGGTT TTCTCTGGTCATAGAACTCTTAAAGGGAAATCATGACAGATTTTCTTGGCTTTA
WI-960b	167 C T ---	---	TTGCTTCAAAGAAGTTCTTGTCTCAGGAAGTTATTCATTGACCAACCTAAAATTTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAAATTTATCAAAGATGTTAAGTTATCTTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	TTGCTTCAAAGAAGTTCTTGTCTCAGGAAGTTATTCATTGACCAACCTAAAATTTGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAAATTTATCAAAGATG/AJTTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTATTATGATGTCCTAGGTACATTTGTTTTATTGTTCTG CGAATGTGTATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTTCTGTGTTTC CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAATNTG

WI-1147b	204 G A ---	---	TTTGCCATTATTTGAAGATAACCCACACACCTTGGTGTCCAGGGTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCGCAACTTCTCCTCCTCCTGCTGCGCTC CTGAGCCAAAACAGGCAATTACCATAAATCACCTTGTAGGATGAACCTTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAACACTCTCATCAGGCAGA
WI-1158b	147 C T ---	---	GCATTAGAGGGTTTCGTTAATGACATTCACCTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAATACAATGTGATGGTCTCCTGAGTGTCTGAATGCGCCAGGTGGC TAAGTCTGGGG[C/T]CTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 C G ---	---	GCATTAGAGGGTTTCGTTAATGACATTCACCTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGT GGCTAAGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 T C ---	---	AAGTTACAGAAAAAATACAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCOCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATGN[T/C]GNCANT AAAAATGATTTGAAATGGGAATAAAGCCCTCCCTCTAATGATTTGACAGGTAGACCTTGCCCTAG GCG
WI-1305d	202 C T ---	---	TTCTCAATCCCAATCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305c	46 C T ---	---	TTCTCAATCCCAATCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305b	153 T C ---	---	TTCTCAATCCCAATCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAA[T/C]TNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305	202 C T ---	---	TTCTCAATCCCAATCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA

WI-1306b	248	A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGTGNNNNNTNG GGCTGGGTGACTGTCCTGGTCAATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCTA/G/GC
WI-1306	240	A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGTGNNNNNTNG GGCTGGGTGACTGTCCTGGTCAATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTA/GTCTTCTAGC
WI-1307b	118	T C ---	---	GACAAGGCTGGTACTAGTTTCCAATTCCTCAATCTATGTACACTTCTCTCAAGTGGACA GATTTCTGCATTATACCTGCTGGGTTGGGGAGCAGTGGTAGGCAAT/CJGTGAGATTGCTTT CCTACCCTCTAAATGTATCTTNCATAATTATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCCTTTGGTGTGTTGTTGCTGTTGTTTCTCTCTGTAAGNTGTTT
WI-1307	118	T C ---	---	GACAAGGCTGGTACTAGTTTCCAATTCCTCAATCTATGTACACTTCTCTCAAGTGGACA GATTTCTGCATTATACCTGCTGGGTTGGGGAGCAGTGGTAGGCAAT/CJGTGAGATTGCTTT CCTACCCTCTAAATGTATCTTNCATAATTATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCCTTTGGTGTGTTGTTGCTGTTGTTTCTCTCTGTAAGNTGTTT
WI-1325b	169	T C ---	---	GAGAGATGCCAAGACAAGCAGAGGGAGAGAGCAACCCNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCTTGTCTCTCT/CJACCCCTCAGAACCTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165	C T ---	---	GAGAGATGCCAAGACAAGCAGAGGGAGAGAGCAACCCNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCTTGTCTCT/CJTTCTTACCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162	T C ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAGAAAGTCTGTATTGTAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTAGTNCATATTCAGGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG/CJGAAGTTGGGTAGTACCAAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCCATCTCTAAG
WI-1327	175	C G ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAGAAAGTCTGTATTGTAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTAGTNCATATTCAGGACAGGCTGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGT/CJGTACAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCCATCTCTAAG

WI-1341b	136 G A ---	---	TATCAGCATGATTGGCTGTTGGACACAAAGTCAATTTGTACTTTTGTGNTGNNNTCCTTTCTCTNTT ACCTGATCCACTATCTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTTNAATTATACCCAAGC [G/A]GGATTGTGATGGATCTGTTATTTCTCTGTCTTGGAAACAGAGAGTCTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCAGCCACCTTGCACTTAGCAAGTGT
WI-1349e	192 G C ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATA
WI-1349d	264 C A ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGATAGTCTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349c	192 G C ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATA
WI-1349b	264 C A ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGATAGTCTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349	264 C A ---	---	CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCAGGTGGTAGGTCTGGCCTGTCAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGATAGTCTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAATATGATAGAAATTTGGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1403b	57 C T ---	---	TGGTATTGGAATGGGTTTCAGACTCCGGTTCTGGCTCTGACCTTTGGTAAGTTGCTTCTCCGAAT GCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATTTCTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTCA TAATCCCAAGTGCCAAAAGGGTTGTATCTGATTGT
WI-1403	58 T C ---	---	TGGTATTGGAATGGGTTTCAGACTCCGGTTCTGGCTCTGACCTTTGGTAAGTTGCTTCTCCGAAT TGCCACTTTATAAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATTTCTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTC ATAATCCCAAGTGCCAAAAGGGTTGTATCTGATTGT

WI-1417c	31 C T ---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGCAGATGTGAGCCCCACGGG GGTACAGCATGCTGCTGGCATTGGAGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTTCGGAAGTTAAGGGCTCGCTTCAAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGCGAGGCCCTTAGTCCGTATTAAATGTTGCTTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGCAGATGTGAGCCCCACGGG GGTACAGCATGCTGCTGGCATTGGAGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTTCGGAAGTTAAGGGCTCGCTTCAAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGCGAGGCCCTTAGTCCGTATTAAATGTTGCTTTGTAGAAAAAGTCGC
WI-1729	172 A ---	---	CCATGAGCAACAGCATGTTTCTACTCTGTGATGTGTATGTTAGGGGGCATGTATATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTCATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAAGA TGTTGGAGAACTGAAAAGAGAGACTTACATGACCCCAATAGCAAACTCCACACATTTCCAGCA GATGTATGTCTCTCGTGGTNACCTCTCTCCACCATCACCTGTGTTTTT
WI-1732b	122 T C ---	---	TGCCTTACTCTTTGTTTCATCCCAACCATTTACATTTTGTAATTTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGGTCAACCCCTTTT/C/ATTCAGTCT CTGCCACATGTCTAGTAACGTGAGTGATGGTGTCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114 C T ---	---	TGCCTTACTCTTTGTTTCATCCCAACCATTTACATTTTGTAATTTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGGT/C/TAACCCCTTTATTCAGTCT CTGCCACATGTCTAGTAACGTGAGTGATGGTGTCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1750	97 A G ---	---	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTTCCCAAAAAAGGTTTAAATCTGTGTGGA CATAATGTTGAATTTGCAGTTTCACTTGG/AGTTTAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAACCGGCTTGCAGTCCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	GGTACACAAAGAAATGCTTCTGGAATCTAC/AGTTAGCGCCCTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCAACCATGAAGCTGGGCAAGAACAAATTCCTAGGAAAAGTACAATTAC TGGAAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCTCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAAGAAATATCATAAAAAAT
WI-1803c	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGTTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGAT/AGTAGGTAGGATGAGCATCACACTTGGGAGGACATATTCTGGAGTNAGATATCCTG GGTGCTAAATTTCAAAATATATCTACTAAAGCATGACTTCTAGAAAAATTAATTAATCTTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAAATAACTGGAATCA

WI-1803b	77 A G ---	---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTTCAGGCAGAA CCATTATGATAGAGTAGGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAAAATATATCTACTAAAGCATGACTTCTAGAAAAATCTTATCTACTCTTGCTCTCAA GGAAATGGGAATACCTATAATACAGTCTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ---	---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGCCGTTTATAC[C]/TGTCTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGGAACGTTTAGCTTCTGCTGGCT
WI-1837	112 C T ---	---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGCCGTTTATAC[C]/TGTCTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGGAACGTTTAGCTTCTGCTGGCT
WI-1840b	79 G T ---	---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACCT[G]/GAGAACTCTGAATATTAGCACATACAAGTGTGACAAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCCCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACCT[G]/GAGAACTCTGAATATTAGCACATACAAGTGTGACAAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCCCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	---	GGGCTCACTTTCATCAGAGCACATATCAGTGTAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTT[C]/TGTCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ---	---	---	GGGCTCACTTTCATCAGAGCACATATCAGTGTAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTT[C]/TGTCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCCCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ---	---	---	TGTTCTCTGGTCCAGGACCCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C]/TGTCTGAGAGGT AAAGTGCCTGCCCAACGGCGACAACTAGAGAGCAGCCAAACAGGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAAGTGCATGAGAAACCACTTTTCTTGTCTCC



WI-1900	119 C T ---	---	---	TGTTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCATAATGGAATATCAACTGGACAACCCCG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCAACGCGCACAACTAGAGAGCAACCAAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTTAACTGCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165 C T ---	---	---	ATTCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCAATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCCAAGTGGAGATAGTGAA TACAGGCAACCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165 C T ---	---	---	ATTCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCAATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCCAAGTGGAGATAGTGAA TACAGGCAACCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164 C T ---	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGAGGATCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAATAAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTTGTTCTGAAAACTTAAATGCACCTCCCAACTTT
WI-1960c	270 A T ---	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGAGGATCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAATAAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTTGTTCTGAAAACTTAAATGCACCTCCCAACTTT
WI-1960b	270 A T ---	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTCATAGAGTNTGTTTGTAGTCTCGTAATAACTGTTGCCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAAGCCTTTCCCATCGAGTGATACAGTACTTTCCAGTTATGGAGATTTT /C/TAAACAATCAAACTGGCTGAGGCTGTTGG
WI-1977	203 T C ---	---	---	AAATCTAGAGCCAGAAAGTCAGCTCACGATTTATAAAGTTGAAGTAATGCAATGTAGTTTCATGT TTTCTCTTAATCTGCACAAACTAGCTAAAAATC/T/CJTAAATCAGTACCAGAGGCAATACCT GGGTTAATGTAAAGCACTCAAAAGTTATGTAGAGTAGTGTCTCTGAGTCACTTTTTTCTACTCTCATT GGCTTCACCAATGCTTCCACTGGATC
WI-2012	102 T C ---	---	---	

WI-2013	127 C T ---	---	C T T T T A G A G T G T C A T T T C G G T T C C C T T C T G G A A G T G A T T C G T G T T A G A A A A A T A G A T G C A A C G T T G C T A A G T A C C T A A C A T T T A A C A G T C T C C A G C A G A T A A T G C T G A T A C T G A C A C T C T C T C A C C A G A A A G A A A T A C C C A T C A T G A G A A G A G A A T G A C T T T T G T C A G T A T G C T C C C G G T C C C T T C A C T G G A G G A T A C T C A G C T T C T G A G C C C T G G T A C T G C A A T C C
WI-2032c	166 G A ---	---	A C C A G A C A T C C C A T C A G G A G T A G T C T T C T G G C A A G C C A G C C C T T C T G A T T C C C A A A A C C T C A A T T T T T C T T N A C T T A C T C A T A A T T G C T A G G A T A T C C A C A T A A C C A A A G C C A A C C T A A C C A C A T C A C C C A A C T G T T T C T A G A T G T A C A C G A J T G T G G A C C T C T G T C T C A A C C T C C G A C T T T C A C A G A T C A T T G G T A G G C T C A C C T C C T G T A A T T G C T T C T G T T T T C A A A G G G
WI-2032b	219 C G ---	---	A C C A G A C A T C C C A T C A G G A G T A G T C C T T C T G G C A A G C C A G C C C T G C C C T T C T G A T T C C C A A A A C C T C A A T T T T T C T T N A C T T A C T C A T A A T T G C T A G G A T A T C C A C A T A A C C A A A G C C A A C C T A A C C A C A T C A C C C A A C T G G T T T C T A G A T G T A C A C G T G T G G A C C T C T G T C T C A A C C T C C G A C T T T C A C A G A T C A T T G G T A G G C T A C G C T C C T C T G T A A T T G C T T C T G T T T T C A A A G G G
WI-2032	219 C G ---	---	A C C A G A C A T C C C A T C A G G A G T A G T C C T T C T G G C A A G C C A G C C C T G C C C T T C T G A T T C C C A A A A C C T C A A T T T T T C T T N A C T T A C T C A T A A T T G C T A G G A T A T C C A C A T A A C C A A A G C C A A C C T A A C C A C A T C A C C C A A C T G G T T T C T A G A T G T A C A C G T G T G G A C C T C T G T C T C A A C C T C C G A C T T T C A C A G A T C A T T G G T A G G C T A C G C T C C T C T G T A A T T G C T T C T G T T T T C A A A G G G
WI-2054b	188 C T ---	---	C G T T T C T T C T A C A T C T T G G G N A C A T A A A G A N G A A G A A G A G N A G C T G C T T T T T G G G T A G T T T G C T C A G A G C T G C C T A G A G C N A G G A C A A G A C A G G T G A C C T T C A A A T A C C T T A C A G A C T T A G G A T T G G A T T T C A T G T G T G T T G G C A G C C C A G G C T C A C A G A A C T A A T A C C T G C T G T C J T T C T G C C T C C A C C A G C C C T A C T C T A G G C T C A A G G A A T T T A C T G G A T G G G C T G C T T T
WI-2054	183 T C ---	---	C G T T T C T T C T A C A T C T T G G G N A C A T A A A G A N G A A A G A A G A G N A G C T G C T T T T T G G G T A G T T T G C T C A G A G C T G C C T A G A G C N A G G A C A A G A C A G G T G A C C T T C A A A T A C C T T A C A G A C T T A G G A T T G G A T T T C A T G T G T G T T G G C A G C C C A G G C T C A C A G A A C T A A T A C C T G C T C J T T C C T C T G C C T C C A C C A G C C C T A C T C T A G G C T C A A G G A A A T T T A C T G G A T G G G C T G C T T T
WI-2573d	129 T C ---	---	T G G G A T T A A A C C C T G T T T C T C C T C C C A G T T C A G T G C C T T A A T G T T T G T G T A G A A A T T A A C A T T A A C A G C A G T A A A A T A G C T C T T A A A T G C A C T T G C C G T T C A C A A G G T G T T C C G T G C T T T C J T G A T A T C A T C T G A T C T T C C C A C C A G G C T T A T T A T G C C T A G G T A A G G G T A A G C A A C A G A G G C T G T G T G A A G T G A A T G A T T T G C T T G C A C A A G G T C A T A T G G C T G G G C T T G G A C G A G
WI-2573c	165 A/C ---	---	T G G G A T T A A A C C C T G T T T C T C C T C C C A G T T C A G T G C C T T A A T G T T T G T G T A G A A A T T A A C A T T A A C A G C A G T A A A A T A G C T C T T A A A T G C A C T T G C C G T T C A C A A G G T G T T C C G T G C T T T T G A T A T C A T C T G A T C T C C C A C C A G G C T T A T T J A G J T G C C T A G G T A A G G G T A A G C A A C A G A G G C T G T G T G A A G T G A A T G A T T T G C T T G C A C A A G G T C A T A T G G C T G G G C T T G G A C G A G



WI-2954c	49 T A ---	---	TTAGCACATATCTGTGTGGGACTTAAGTACAGACAAGGCATATAAAAAA[7A]CAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACACATATCTGTGTGGGACTTAAGTACAGACAAGGC[7A]GTAATAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACATATCTGTGTGGGACTTAAGTACAGACAAGGC[7A]GCATAAAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGAT[C]G CTGCCAGCACCAATAAGCTTTCTTTCAAAACAATTTGTGTAACTCCTCCTTCTTAATAAACCTAAG ATTTCTTTTGTCCCTGACATTCGAAAGGCCACGCTGGTGTAGATGATGCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAAGAAAACCTTTTACTTAGGGATTGTCT
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGAT[C]G CTGCCAGCACCAATAAGCTTTCTTTCAAAACAATTTGTGTAACTCCTCCTTCTTAATAAACCTAAG ATTTCTTTTGTCCCTGACATTCGAAAGGCCACGCTGGTGTAGATGATGCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAAGAAAACCTTTTACTTAGGGATTGTCT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCG TCCAGTTTNNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTJA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCG TCCAGTTTNNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTJA AATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCG TCCAGTTTNNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTTJA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAGACCCGACCCGAAAGGAGGAGCTGGANTTTTTTNA AATCTTCTTCTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 A T ---	---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAGACCCGACCCGAAAGGAGGAGCTGGANTTTTTTNA /AAATCTTCTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995e	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAGACCCGACCCGAAAGGAGGAGCTGGANTTTTTTNA AATCTTCTTCTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151 G C ---	---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAGACCCGACCCGAAAGGAGGAGCTGGANTTTTTTNA AATCTTCTTCTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133 A T ---	---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACAC ATCTCACTTAGCTCCTTC/TCCTGCCATATCCTGTTTCTTACTCTATCTCCTGAGACTTCTCCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTNNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACCTTGCAAGG
WI-3147	85 C T ---	---	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATTCCTTATTGAGGTCCATGTCCATTACCTCTACTTA T/CJGACAGGAAGAACACACAGAAAGCCTCTGTTTGAATCTGGCTCTTATAAATACCTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT
WI-3234b	68 T C ---	---	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATTCCTTATTGAGGTCCATGTCCATTACCTCTACTTA T/CJGACAGGAAGAACACACAGAAAGCCTCTGTTTGAATCTGGCTCTTATAAATACCTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT
WI-3234	68 T C ---	---	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATTCCTTATTGAGGTCCATGTCCATTACCTCTACTTA T/CJGACAGGAAGAACACACAGAAAGCCTCTGTTTGAATCTGGCTCTTATAAATACCTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATACATCCTTAATAAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT

WI-3292b	106	G A	---				GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCTCCGTCOCCAAAGCCTATGTTACTGTATGCTG/AJGGTATTGGATGGGATGGATTACTT GCCATGAATATTTTCCATTGTTCTCATTAATGATTAATTAATTAAGTAAATATTATTNCCATGA GACACAATGGAAAAATGGAAAAACATTTCATGGAAAAAACCCATTTCATC
WI-3292	106	G A	---				GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCTCCGTCOCCAAAGCCTATGTTACTGTATGCTG/AJGGTATTGGATGGGATGGATTACTT GCCATGAATATTTTCCATTGTTCTCATTAATGATTAATTAATTAAGTAAATATTATTNCCATGA GACACAATGGAAAAATGGAAAAACATTTCATGGAAAAAACCCATTTCATC
WI-3355	19	G C	---				CCATGAACCATGGGCTACA/GC/JATATCTCTAACTTCAGAGTCCCTCTACTGGAGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATACTATTCTTCCAAGCCTTAAACTCATCAGAA AAAAAATCATCAAAAAAGTCGAAGTAGTTTINATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGACTTTNAGTTG
WI-3408	194	G A	---				CCATGAAGAATGAGTTCCTCCCTCCCTGGGTCACGCTAAGAATAGCACACCCCTTGAGAAATTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCTCCGCTCTAAGACACACCTTTATGCTTTCNAAGCTTT CTGGAATTGGGATGAATCINACATTCAATGTGCACCTTCGTTGGGATCACTTCTCC[G/A]TGCCCC ATCTCGNAGAAGCCACTGGGAAGTCGAAGGAGTCACTTCAATCAGG
WI-3505b	131	G A	---				TAACTTATGCCCTCATCTGGCTTACTGCTTAGTCCCATTTTGTATCATGAGTGCACCTTAAAAAATTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANNGGAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTGCATAT
WI-3505	131	G A	---				TAACTTATGCCCTCATCTGGCTTACTGCTTAGTCCCATTTTGTATCATGAGTGCACCTTAAAAAATTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANNGGAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTGCATAT
WI-3564b	177	C T	---				GCTAGTAAGGTTCCACCTAAATGGTCCCAAGTCAGGAGAGTCACTAAATGTTTTGAGAAATAAAGT GAAATCAATGTGCTTCCAGTGTATTACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTC/JAACAAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTCACAAAAACAAA
WI-3564	177	C T	---				GCTAGTAAGGTTCCACCTAAATGGTCCCAAGTCAGGAGAGTCACTAAATGTTTTGAGAAATAAAGT GAAATCAATGTGCTTCCAGTGTATTACATGGCAGAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTC/JAACAAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTCACAAAAACAAA



WI-4110	130	T C ---	---	GAAAATGATGTTTTGATTTCCCTTCTATCTTCAGATTATTGGAGTGTCAATTAGAAAACCTGATAGT AACCTTTTATTGATGAAACTCTGTCTATAATTAAACCTTCTCTTCCTGCTTTATTTTGGCTTC/JACA GTTTAGGTAAATAAAAGATGCCCAAGAAATTCAGTATTCAGTACAGTAAAGTAGCAACCATGGG GTAGGCAAGTNCAGAAAAGGAGGAGGNGGGGGTTTTCTGGGAAGA
WI-4119b	168	G A ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGACAGGACAAGACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168	G A ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGACAGGACAAGACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51	T G ---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[T/G]TTAAACTATTT CAAATAAACATAAAGAAAACATGATGAAATTCCTCGTTACATAATTGTATAGAATTTAGTGGG TTCTTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGTTGGATGTTTCTATGCTTTCTC AGGCACAAACACAGTGAAGAACCCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51	T G ---	---	CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[T/G]TTAAACTATTT CAAATAAACATAAAGAAAACATGATGAAATTCCTCGTTACATAATTGTATAGAATTTAGTGGG TTCTTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGTTGGATGTTTCTATGCTTTCTC AGGCACAAACACAGTGAAGAACCCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145	G C ---	---	TTGTACATGTTTCATTCATCCCTCCCATCTTTCTGTCTTATAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATAC GTGCTGT[G/C]CCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTAAGTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137	T C ---	---	TTGTACATGTTTCATTCATCCCTCCCATCTTTCTGTCTTATAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATAC TTC/GTGTGCTGCGCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTAAGTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188	G A ---	---	TAACACACTTTTCATTTGGTTTCTTATCTGAGTAAAGGACCATCCATTATATACAATCCCTC AGTTCTATGCTTTAGAGTACTATAGGACTACTGTAAATTTAGAGGGAATTAATCTTGGAGTA GGGGAATGAGTTAAATAATCTACCATGCCAATTCAGGGGACTGTGGTTAA[G/A]ATGCTCTCTCT TGCCCCCTTCCCAAGTCTTAAATCTCTAG





WI-4584	144 A G ---	---	TTGGTGGCATTAGCCTCATAACAACATAATTTACAATCATAATTTGTTACTCTTATTTTACAACAAG AAAAATGAGGCTTAACATCACACCTCTGCTTAGTCGAGAGCCAGATTTGAACCCAGGAATCCATT CACCGGTACAGJTGCTACCTGGGTAAAAAATGTTTAAATTAATCTATGGCATTAGATTTCAAAGA GTCTAATGTGGTTTGAATAAGGTGCTTAAATTTGTTATCAGTAIGC
WI-4639	185 C T ---	---	TTCTGCAATTTGAATGTATGGTCAGACTTCAGAGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTAACCTTTCCAAATCCACCATTTAC TGACCATATGACTTGGGGAACATATCTCACCTATCTGAGTCTGTATCCQCTCATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63 A ---	---	AAATGAATCCGCTTTAGAGCAATAACAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGA[A/- ]GATTACTCATAAAAGCATATAATTTTATAATATGGAATAATTAAGTAAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTAGGAGGAGGTAGTTTCTACTTATAGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCCGATGACAATGATGAATGTTCTAAGCAGACAG
WI-5390	87 C T ---	---	GCCTTTGAGAATGAAAAGGGAGCCTGGACCATTCAGGGCTCTCTCATCTCTGATTATTTTGTGTAT TTATTGTTCACTTATTATCTGCTCTCCCTCTCTGGTATGCTTGTGTCATGAAACAATGAATTC CCCAGTGCCTGGCCGATTCTGGCTCTAGAGGTGTCAGAAAAAAGTTTCGGTGAATAGAAATTG ACGAATGGTTTCAGAAATGAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87 G A ---	---	CCCTGGCTGCTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAGAAATCAATTTAAGCAGT GCAACATTATTTTAAATTTG/AJAAAGAAACTTGTCTGAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGGTGAATCCACCCCATCTCTTTCCACGATAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTCATAACAA
WI-5404	87 G A ---	---	CCCTGGCTGCTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAGAAATCAATTTAAGCAGT GCAACATTATTTTAAATTTG/AJAAAGAAACTTGTCTGAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGGTGAATCCACCCCATCTCTTTCCACGATAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTCATAACAA
WI-5545b	77 A C ---	---	TAGGAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATTCTTCCACCTCACACTGCCGCCA TATCTCCTC/AJCCCAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAAATGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTATTTTCATTICA
WI-5545	77 A/C ---	---	TAGGAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATTCTTCCACCTCACACTGCCGCCA TATCTCCTC/AJCCCAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAAATGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTATTTTCATTICA

WI-5860b	134	A G ---	---	ACTCAAGTTGGGGGATAAATCAGAAGTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTACTCCCTAACCAACCTTCTAACTGAGGAACCTAC[A/ G]TTATACTGGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A G ---	---	ACTCAAGTTGGGGGATAAATCAGAAGTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTACTCCCTAACCAACCTTCTAACTGAGGAACCTAC[A/ G]TTATACTGGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C G ---	---	GCAACAACCTATTATACCTGATCCAACCCAGGTCTACTAACATTAATCAACCCTAACCACAATAC TATATATTGCTCTGTTCTGAATTATTTTCAATTAGAACTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGTCCAGGAGTCTCAATGTGAAGTATAATTTCTTACAGAG TAATT[C/G]ATAGTAGGTCAACCAAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C/ A]ACCCCTATATTNCTGTCCTGTGCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAAATTTTATACCA
WI-6109c	147	T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCCCTATATTNCTGTCCTGTGCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT TGNAAAATTATCCCTGAAAATTTTATACCA
WI-6109b	147	T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C/ A]AAACCTATATTNCTGTCCTGTGCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAAATTTTATACCA
WI-6109a	129	T C ---	---	AATGCCATACACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTAGCACCTGTC TTCCAACACATGCTGTTTGTTCATGAT[C/G]GCATATCCCAAGTGCCCTAGACAATGCCTCCCATAC AGTGAACAGATTGTGACTAAACACATACCTTGTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6112	96	T C ---	---	

WI-6244	103	T C ---	---		TAATTGCACAACCTTACATATCAGGGTTTCTGATTTGAAGGAAGAGAATATTCCTTTCTTTAGTAGTAT GCTTAATATTAAATTCATAATAAGTGCACCATCTCTT/CJGCTCCTTATAAATGTGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAAGCAACCCAGGAGACATTTTATATACTCTACAGTGGGGAAGACTT CCTATTTCTTCCCAAGGATGGATACATTCTAC
WI-6268	124	C T ---	---		CTGGCCTTATAATCCAAAGTTAGGATTAACTTACCCCAACTTAATAGACTTCCAGACAGATTGCAGTT GTCTACAAGATTCTCTCTAGTAGGGCTTTGGGTGTGGCACCCTTTGGCTCATT/CJTACTCTCCCT GGGTCTATTGACTTTCAGGGAGCCTAGAAGAGCTGGACAAAACCTGCTTCTTTGCAGAAAAGATCG GGGTCCAAAGATTTCGTACGATTTTATA
WI-6336b	234	C T ---	---		AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTCAAGGGCTGAGAGAGCTCACTCCCCC ATATAATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATTGTG GTACCCCAAGTGCATTATGCTTGGTAGAGCC/CJTJGAGGACACTGACAGT
WI-6336	234	C T ---	---		AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTCAAGGGCTGAGAGAGCTCACTCCCCC ATATAATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATTGTG GTACCCCAAGTGCATTATGCTTGGTAGAGCC/CJTJGAGGACACTGACAGT
WI-6381	92	C A ---	---		TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAAATTAGTTATGAGTATTTATACAATTA CAAAAAATGNTTCATGTTTTAACAA/CJA/GTATTTTAAAGCTCAAAACATTTTAAACACAGGCACAA ATTCTAANGGCATATGCATTCACCATGGCTTTTGAATGTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGCAAAAGATCAGAGTTCCAG
WI-6436	198	C G ---	---		GGTTGAGGCATTGGGAAGGCAGAAATTGAGGCAGTAGAAAATGGACATTTTAGGAAAGAGAAGT TCAGAGCAAGTCATGACAGACAGGAATACAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTCTATAATAAGAAGTTAGACTTTGGGTGTAGTAGTTGTAGTAGTAGGTAGCGTT/CJ GIATTGGGTGTATTCACAGACAAGGTGATGTTCTAAGATTTGATATTATTG
WI-6449	186	C T ---	---		GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTCTACACTGCCAGATTGTTAAATTTTGAATAATC GTATCTGGTTCTATTTCATCTGCATCTCTGATCTTATGCTGGCTCTATT/CJATCCCTATTCTCTGA TCATTATGTCAGACCTGAAGTTCTCTCTAAATTTTCTGTGGTGTATTATA
WI-6449	186	C T ---	---		GAGGCCTTTTGTCTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGTTCTGATTGGTTGGTGTCTACACTGCCAGATTGTTAAATTTTGAATAATC GTATCTGGTTCTATTTCATCTGCATCTCTGATCTTATGCTGGCTCTATT/CJATCCCTATTCTCTGA TCATTATGTCAGACCTGAAGTTCTCTCTAAATTTTCTGTGGTGTATTATA

WI-6463	72 T C ---	---	GCTGGAGAGAAAAAGACCTCCAAAAGAGAAACTAAATCAGAGTCTCTTGAGCAAGGAAATTGAAA AGAACAT/CJTGAATAAAATTAAGTAGAACTCAAAGAGCCAAAAGTCCCAATTGTGTCCATTA TAAGAAATATTTGAATGGAATCTTAAGAATGATTTTATGATCAGTTAAATGTTCTTCTCCTCCTC CAGTCCCATTTATATGACATTCGCGATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTTCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAA/CJTGTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGACTAGAGGAGAACTATGTAAAGCAG AGGTATAGAGGAACATAAGTATAAAGAGTGAGGCCATACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTTCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAA/CJTGTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGACTAGAGGAGAACTATGTAAAGCAG AGGTATAGAGGAACATAAGTATAAAGAGTGAGGCCATACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACCTCAATTAACCTTGGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCAGCTTCGAGGCCGTGCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGATCAGAGT/AJGCTCCTTGTGAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACCTCAATTAACCTTGGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCAGCTTCGAGGCCGTGCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGATCAGAGT/AJGCTCCTTGTGAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTGAATGCAACTGAGAAANTGGTTTTNTAGGCCTACCTTTTATTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA/GAJTCAATTTTAAAAAGAGAACAGGAAATAGGAAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAACTTATCAGTCTTC
WI-6564b	54 G A ---	---	TTCTTTATGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGTCTGTGCTGAAATCTCAATTAATTTCTCCNCCTATTCCTTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAGACCAACA
WI-6564	54 G A ---	---	TTCTTTATGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCATGC[G/A]CACTGGCTTTG TAGGCATTACATCATATGTCTGTGCTGAAATCTCAATTAATTTCTCCNCCTATTCCTTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAGACCAACA

WI-6608b	46 C ---			CTAATCACAGTAGCACTGAACATGGCTCTAGTGAAGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTCCTCTAGTCTCTCCCTAGAGCTAAATATGCACTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCCAAAAAGAAAAACACCTGTGCCAGGCACCTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6608	46 C ---			CTAATCACAGTAGCACTGAACATGGCTCTAGTGAAGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTCCTCTAGTCTCTCCCTAGAGCTAAATATGCACTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCCAAAAAGAAAAACACCTGTGCCAGGCACCTAGCTACAAGGCCACACCCAGAAAAAGGAA AGC
WI-6666	68 C A ---			GTTAGACAGTATCCAGCAAAAAGGTTATTTTATACCTCTACTTTTCCAAACGAGGAAACCTCCCC AIC/AJAAATCCCATCAACACACAGATCATGCTGGAAGGCATTCGTCTACTCTGTGGTTTCATGTAA ATGTTGGGGTGAATCATTCCGCTCTCTCTCTCAAGTTCAGGCTCTTGGGTAGACCAAACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G ---			AGATTAAACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCCTCTCAACAGTAAGCACACAATGAACI/AJTTGTTAGCCA GCATTGCCATTGAGGGCCGAGTCAAGGTTGTGGGCCAGAACTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTTGAACACAGACACAGAACTTTAGAAAGGGAT
WI-6670	120 A G ---			AGATTAAACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCCTCTCAACAGTAAGCACACAATGAACI/AJTTGTTAGCCA GCATTGCCATTGAGGGCCGAGTCAAGGTTGTGGGCCAGAACTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTTGAACACAGACACAGAACTTTAGAAAGGGAT
WI-6704c	33 T C ---			TTTGAAAAATAAATTCATGCACCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTACAAATAAGTTTTTCATGACACACGNC CTATTGCTCTTTAAATATGTTGTACATGTCATTAATCGATTTCCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C ---			TTTGAAAAATAAATTCATGCACCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTACAAATAAGTTTTTCATGACACACGNC CTATTGCTCTTTAAATATGTTGTACATGTCATTAATCGATTTCCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C ---			TTTGAAAAATAAATTCATGCACCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTACAAATAAGTTTTTCATGACACACGNC CTATTGCTCTTTAAATATGTTGTACATGTCATTAATCGATTTCCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ---	---	CCATGGACAGTTAAITTAGGAAGCTTCGACTTGTTAGATAACAGAGGAAGTCCCGAGTTATCTACCT ATTCCCTAAACACACATTTTGTGAGGCTGGAATGATCCCG/ATAGTAAACCTCAACATCCACACCT GCATAAACATCGCCTCCCAAGTGAATTTATTTACTGAGTCGACACAGGATGTCACCAGTGAGCCTC ATCTCCAGTCCATGGAGGAGTTGACTTAGAOCCTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C ---	---	AAACAAATGGTGCATTGCATAATATTTGGTGCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTCTTTGTCTACGGAATNCTGCAGATCCTTATGT GCCACACTTAAAN/GC/AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAATACCCAAATCCAGTTCCCTCTTC
WI-6766	148 G C ---	---	AAACAAATGGTGCATTGCATAATATTTGGTGCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTCTTTGTCTACGGAATNCTGCAGATCCTTATGT GCCACACTTAAAN/GC/AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAATACCCAAATCCAGTTCCCTCTTC
WI-6787b	97 A G ---	---	ACAGATAAAAGTCTTTATCCCTGTATGTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACTTGTGAGCAATGTTCAAATTCACAG/TTTTTACTGCATAAGATATCTTCATGTACAACCTGT ATGCTTTGCTCTCTTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAAGGA GAGTGCAATAGGGCAGAGTAGANTACTACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G ---	---	GAACCCACAGGTCCTGTTATTTAAGGAGCATTTACATTTAGTAGCAAGTTTCAACACACATTCA TCAACAAGGCGGTCTTCAAATCAATCAGTCAACCCCG/CG/AGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGGCTGTAGGAAGTAGGTTAATGCCCTCTAATCCCCGGAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37 T C ---	---	CACAATAATAAATCACTCCCTACCCTTGAAACCTTTAT/CJAGAAGCATTTTAAATTTTACAACACA AAGCTCAACGNCCTACAATAAGTCTAGTGTGTACGNGCCAGGGATAAGGCTGAACAATA AATTAACCCCTTAAATGCTATGNACAAGTACAAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---	---	CACAATAATAAATCACTCCCTACCCTTGAAACCTTTAT/CJAGAAGCATTTTAAATTTTACAACACA AAGCTCAACGNCCTACAATAAGTCTAGTGTGTACGNGCCAGGGATAAGGCTGAACAATA AATTAACCCCTTAAATGCTATGNACAAGTACAAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---	---	GCATGATTAAACCAGTGCAGAAAATACCAAGTACATTGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACAATGATAGCT GCAGGTAAC/C/ATGTGGATACCCCTGTGTCTACTNGCCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTTCAAACTTGGTTCAAGGTGGGCTGTGCAG

WI-6817	145	C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTTGCTTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC[C]/ATGTGGATACCCCTGTGTGCTCTACTNGCCCTCCAAGGCATTGAGGGGATCATCAAAGATGTTGGACACCTTGTTCAAATCTTGTTGAGGTGGCGCTGTGCAG
WI-6819b	221	C ---	---	GATGGAAGGCCATTTATTTTCTCTAAATTTTAAAAATAGAAGACTTTAATGTGAAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCCGTCAGTAGTACACATTTCTCTATGGTCTCTTCAACAGTTTTCATATACAAAAATTTTCTGCTATTTTGCTTAGCAAAACAGCAATAACTTTTGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175	G T ---	---	GATGGAAGGCCATTTATTTTCTCTAAATTTTAAAAATAGAAGACTTTAATGTGAAAAACATTTAGTACCATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCCCGTCAGTAGTACACATTTCTCTATGGTCTCTTCAACAGTTTTCATATACAAAAATTTTCTGCTATTTGCTTTAGCAAAACAGCAATAACTTTTGTTTCTCTATATGACACCTAATAT
WI-6826b	154	A G ---	---	GCAAAAAGCTTTATTGGCTCCAAACAAATATCCCTTTTAAAACTCCTCTCTCTCTCTGGTCTCAGTGGAAACAACACATTTGAATTTTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATACATGCAAAAACCTTGTACAT[A]/G/GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGTGGCACTGTTAAGCTGAATTGCAAAATTATGGCAACACACACTGGAGTGGGTATACGTTG
WI-6826	154	A G ---	---	GCAAAAAGCTTTATTGGCTCCAAACAAATATCCCTTTTAAAACTCCTCTCTCTCTCTGGTCTCAGTGGAAACAACACATTTGAATTTTCAGATTTGCAGTTTATAGCATTTTTCCTTAAGAACCATATAAATACATGCAAAAACCTTGTACAT[A]/G/GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGTGGCACTGTTAAGCTGAATTGCAAAATTATGGCAACACACACTGGAGTGGGTATACGTTG
WI-6857a	122	T C ---	---	AGTGCAAACTATTTGAACAAAAGTAACTATGAGTCACAGCATTCAGCAAGACATCAGACACCGGAAGAGTGAAACAATATTCACCTAAGTAAATACAGCAGATGAGATGCTCTCACATGTAT[C]/ATTTAATTATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTTCAGTGTAAATTCACAAATATATAGCAGCTCAAACACAAATGCAGGAGCACAATGGCAAAAGTTTGGCACTGTTTGGGCTAAAT
WI-6865	153	G A ---	---	TTATAGAATACTTATGGGGCATAAGNGTAAATGAACCTGTCAACCTTAAATCTAAACAAACAGCTTGTTTGTGGTTGCTGCTGAAATCCTCCCTGCTCACAAAACAGCCAGCTACTNGGTTTCTAAAAGACGTAATTTGCAGGCAAACTTC[G]/ATAGAGCCATTCGTGTGCAGAAAGGGAAGGAGAGCTGTTGTTTACCTGTAGTATGAAGATATCTTTGCGCTGTTAGAACTGAGCTCATTA
WI-6909	73	C T ---	---	ATTGAAAACCTGGTAGCAACAGATAAATTACAATAGAGCCTGGATATAAAAATGAGAGAAGAAATGCAGACTT[C]/TJAGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTTTGAATCAGATTTTATGATACGGAAAAAAAATTTCCTTTTTTTGGCAACAGGATTAATTCGAATAATAAATCTGCCAGTGCCCAATCAGAAACACCATTTCCACAATATTTCATGATGCCCTAGTTCCTATTTTATACATATC



WI-6910b	163 G T ---	---	---	CACTCAAAACCTTTATTCATTGATTACAAACTGTACAATATTTACAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAAATTAATGTGGTAGAAAA GTCAGAGTGGCTGACCACTCCCGAACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144 A ---	---	---	GCTTGTTTTTTTGTGTTTTTAAGTGACACCTTGCCCTTGCGGCATTCTTCACITATCTTACCC AAAGTGCCCTTGGGCCAGCCACTGACTGATTTAAACCCAGAAATGTGTTTTAAACAATGTGGT CGTGGTAATTCAGGTGATTTTNAITTTCTATTTGGTAGTATTTTCAGATTTCCCCACAAAGAACATG TATTGCTTTGTAAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175 T C ---	---	---	CAATCAAAAGTTCCAAGTTTCAAGCTGGGATGAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTNCCCTCTGATCCAGCTGCAGCTCCCATAGAAGTTCACTCTTAATTTCAATGCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGGTCAGCTAAAGGTC/AACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175 T C ---	---	---	CAATCAAAAGTTCCAAGTTTCAAGCTGGGATGAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTNCCCTCTGATCCAGCTGCAGCTCCCATAGAAGTTCACTCTTAATTTCAATGCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAAGGTCAGCTAAAGGTC/AACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79 G A ---	---	---	TTTTTATGAACATTTTCAGATTCCTCATATCAGACACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCAATGTCCTCAATCCCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACATATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTTATGTGAAAT AAGGCTTTAACCAAGC
WI-6955	79 G A ---	---	---	TTTTTATGAACATTTTCAGATTCCTCATATCAGACACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCAATGTCCTCAATCCCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACATATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTTATGTGAAAT AAGGCTTTAACCAAGC
WI-6957	47 C G ---	---	---	AAACTAAAACCCCTTATTGCTCCAAAGTGTGGCAAAATAGAAAATC/GTTCATTAATTACATTAGG AAATCGGTGGATAACGGAGTATAGTTATCCACTTAAGAAGCATTCCAGTCAAAATATACAAAA ACAAATTCAGATTGCTGGATCTGGTCATTTATGGCTGAAGAAGTGGATTGAAAACCCACTTTAGG CTAAAATAATGTATATGAATAATGCATAGACTGTGATCTAGAAAATCATGC
WI-6996c	242 G T ---	---	---	ACTCTAGTGCCTCTGTACCAACCTCTAATGCCCTCTGGTCCCGCACTTCTGTATGTCCGTAGGCCT TAAATCGCTGGGTCCCTCCCTCTGTCTTCAGACCCAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTGCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCTCTCCG/GTGGGATC

WI-6996b	242	G T ---			ACTTCTAGTGCCTCTGTTACCAACACCTCTAAATGCCCTCTGGTCGCCGACCTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGGCTCCCTCCCTCTGCTTCAGACACAGAGGAGGAGAGAGCGGCGAGTTCCTCTG CAGGAGAGAGAGGGGCTGCTGGACCCAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGTCCTCTCTCTCCG/TTGTCGGATC
WI-6996	228	T G ---			ACTTCTAGTGCCTCTGTTACCAACACCTCTAAATGCCCTCTGGTCGCCGACCTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGGCTCCCTCCCTCTGCTTCAGCACCCAGGAGGAGGAGCGGCGAGTTCCTCTG CAGGAGAGAGAGGGGCTGCTGGACCCAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGTT/GJGCTCTCTCTCCGGTCCGATC
WI-7021b	112	G A ---			TGGGAGGACAGGGAGATGCTGCAGTTCCTAAAGAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTGCTGAAAGCCACAGACAATATGGTCCCAAAT/GA/CCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G ---			TGGGAGGACAGGGAGATGCTGCAGTTCCTAAAGAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTGCTGAAAGCCACAGACAATATGGTCCCAAAT/GA/CCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T ---			GGCAGTAGGACACACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGAGTCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/C/TTGGTTGGGAGCCTCT GGGCTGTGAAGTCACCTTGTGTTCCTCAAGTTTCCAAACACAGAAAGTCATTCCTTCTTTTAA ATGGTGTCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7056b	118	C T ---			GGCAGTAGGACACACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGAGTCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/C/TTGGTTGGGAGCCTCT GGGCTGTGAAGTCACCTTGTGTTCCTCAAGTTTCCAAACACAGAAAGTCATTCCTTCTTTTAA ATGGTGTCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7091b	153	A C ---			AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACCTGCTATAAATAGTATTCGAATCACTGTG CTTAATTTAAATAGCATT/C/TTCTATCATTTATCAGCCTTTTATGTATTTTCCAAAGTAAAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C ---			AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACATGTTTATACCTGCTATAAATAGTATTCGAATCACTGTG CTTAATTTAAATAGCATT/C/TTCTATCATTTATCAGCCTTTTATGTATTTTCCAAAGTAAAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT

[illegible]

WI-7175	194 C T ---	---	---	CTCTAGACTAGTGCCTTTACCTTTATTAACTGTGACAGGAGCCCAAGGAGTGTCTCTCACCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATAATGGTTTACTGCTGTCATTGTCATGCCTA(C/T)AGAT AATTTATTTTGATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---	---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTGGCTTTTCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGCTACTGGCTGCTCTAGGGGACAGACCAGTGACCCAGAAAAGCATATAACACCA ATCCCAGGGCTGGCTCTGCACTAAGAGAAAATTCGCACTAAATGAATCTGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A ---	---	---	TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTGGCTTTTCTCTGAGCCCAGCTGCCTGGAG AGGGTCTCGCTGCTACTGGCTGCTCTAGGGGACAGACCAGTGACCCAGAAAAGCATATAACACCA ATCCCAGGGCTGGCTCTGCACTAAGAGAAAATTCGCACTAAATGAATCTGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116 A C ---	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCTT/C/TCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGGAAGCCTAGTACCCCAATT
WI-7182	106 C A ---	---	---	GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCTATCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGGAAGCCTAGTACCCCAATT
WI-7191b	273 T A ---	---	---	ATAATTGCTTGTCTAGCCTGGCAAGATATTTTCATAAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACCACAGCACCACATCTAAGCATTAGTGATGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATAATTTAAGGAG CTCCCAAAATGIGTTACCTATTAAATTTGTAACCTCAGCAAGTAGAAGACCATT
WI-7199c	112 T C ---	---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGACCTATGAGCT/C/GGGGCCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCAATTCCTTAATGTTTGTGTTTGGTGCTGAATTTCTTTTATTAT AGTCCATATAGTTTACTCCTCAGTTCCTCACCATCATCATCTTGCTAA
WI-7199b	112 T C ---	---	---	CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGACCTATGAGCT/C/GGGGCCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCAATTCCTTAATGTTTGTGTTTGGTGCTGAATTTCTTTTATTAT AGTCCATATAGTTTACTCCTCAGTTCCTCACCATCATCATCTTGCTAA

WI-7216c	237	T C ---	---	TGACACTAACACTCTAATCAAGCGAATGTTGGAACACCACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCTCCAGAAAAATACGTATGT TTAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCCTGAGGCTAAACACAGTTTGTITTTTTCCTGTAAATCACCTT
WI-7216b	237	T C ---	---	TGACACTAACACTCTAATCAAGCGAATGTTGGAACACCACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCTCCAGAAAAATACGTATGT TTAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCCTGAGGCTAAACACAGTTTGTITTTTTCCTGTAAATCACCTT
WI-7220b	147	A T ---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCACTATTATTTGCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAA/JTJAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATTTCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7220	140	A T ---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCACTATTATTTGCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGC/JTJTAGAAAAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATTTCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7226	232	C ---	---	GATCGAATTTTCAGATGATTCGGAAATTTTCATTCAGGTAATTTGTAATAGTGACATATATATGTATA TACATACACCTCCTATTCCTTAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTGATCATT CCCTTTCCATATAGGAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGTCAGTGAAAAATAA TTACCCACAAATGCCACCAGTAACCTAACGATTCTTCACCTCTTGGGGTTT
WI-7228b	254	G A ---	---	ATAGCTTCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATTCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTGTCTTTGTAATCTATTTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAGATATCTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAATGTI
WI-7228a	163	G A ---	---	ATAGCTTCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCAATTCATAA TATGTTCCACCAGGAGATTACAAATTTTGTCTCTTGTCTTTGTAATCTATTTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAA/GAJATATCTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAAA
WI-7233c	213	C T ---	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGCTCGGCTGTTGTTGATACATCCATTTTCAATTTGTACA GATGTGAACCTTATTCCTTGTCACTAATTAATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAAGTGAAGTGAATA GTGTAAGTAC/JTJTGACAAAAACCACTGCCAGATAACCCAGAGGGGCTGTG

WI-7233b	213	C T	---	CGATCGTACTGCCAGTAGCATTTGCTGTCTGTCGCGTCTGTTGTACATTCATTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACTAAATATATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTACTTCTCTTGGCAACCTTTTGTGGCAATATTAAGTGAACCTGCTAATA GTGTAAAGTAC/TJGTGCACAAAACCACTGCCAGATAAACCAGAGGGGCGCTG
WI-7233	211	T C	---	CGATCGTACTGCCAGTAGCATTTGCTGTCTGTCGCGTCTGTTGTACATTCATTTCAATTGTTACA GATGTGAACCTTTATTCCTTGTCACTAAATATATTTAAATATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTACTTCTCTTGGCAACCTTTTGTGGCAATATTAAGTGAACCTGCTAATA GTGTAAAGTAC/TJGTGCACAAAACCACTGCCAGATAAACCAGAGGGGCGCTG
WI-7238	128	T C	---	GGGTCTACAGACAGCTACCATTTTGTCTGTATCTGTAAACACITTTTGTCTTAGTCTTTTCTTG TAAATTTGATGTTCTTTAAATCGTTATGTATAACAGGCTTATGTTTCAGTTTGTTC/CJCCGTT CTGTTTTAAACAGAAAATAAAGGAGTGAAGCTCTTTTCTCATTTCAAAGTTGCTACCAGTGAT GCAGTAAATTAGAACAAAAGAAACATTACAGTAGAACATTTATTGCCTA
WI-7252f	520	T C	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCTTCCACTCGACAGACGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGGCCCTGGCTCGAGGCTGCCCGGCCCTGGTCTCTGTCGTCG GACACTCTAGAGAACGCAAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCTCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCCA
WI-7252e	552	T C	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCTTCCACTCGACAGACGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGGCCCTGGCTCGAGGCTGCCCGGCCCTGGTCTCTGTCGTCG GACACTCTAGAGAACGCAAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCTCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCCA
WI-7252d	540	T C	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCTTCCACTCGACAGACGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGGCCCTGGCTCGAGGCTGCCCGGCCCTGGTCTCTGTCGTCG GACACTCTAGAGAACGCAAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCTCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCCA
WI-7252c	552	T C	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCTTCCACTCGACAGACGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGGCCCTGGCTCGAGGCTGCCCGGCCCTGGTCTCTGTCGTCG GACACTCTAGAGAACGCAAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCTCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCCA
WI-7252b	540	T C	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCTTCCACTCGACAGACGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGGCCCTGGCTCGAGGCTGCCCGGCCCTGGTCTCTGTCGTCG GACACTCTAGAGAACGCAAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCTCTCTCTGGAGGATGCAGGTGGAACCTCAGTCAATTAGACTCTCTCTCCA

WI-7252a	520 T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCCCTCCACTCGCAGCAGCGCCGGGGACAGAG GCTGCCCGGGCGCGCAGCCCGGCGCTGGGCTCGGAGCTGCCCGGCGCCCTCTGGTCCG GACTCTCTAGAGAACGCGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAAGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCTTT
WI-7265l	231 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227 T C ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231 T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/AAGGAGTAAGATTTGCCT
WI-7265e	227 T C ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/CJCTTAAGGAGTAAGATTTGCCT
WI-7265d	174 T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAGATTTGCCT
WI-7265c	170 T G ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCATTCTGTGGTTCAATTGTAGTT TAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAGATTTGCCT
WI-7265b	121 T G ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCAATTTACCCATTCTGTGGTTCAATTGTGTA GTTTAAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAGATTTGCCT
WI-7265a	80 T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTCCAGTATGTTT/AJTATTTGCCACCAAAAGTAATGCAATTTACCCATTCTGTGGTTCAATTGTA GTTTAAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAGATTTGCCT
WI-7281b	183 C ---	---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAGTCTGGCCAGCCTGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCCGCGAGGCCGAG GTGTTGTGAAGACCCTGTTCTGTGGTTGGGTCCTGCAAGAAGGCCTCCTC
WI-7281	171 C A ---	---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAGTCTGGCCAGCCTGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC/AJTGGCAAAAACGGAGTCCGCGAGGCCG CAGGTGTTGTGAAGACCCTGTTCTGTGGTTGGGTCCTGCAAGAAGGCCT



WI-7282b	159 G C ---	---	TGTCACCTGGCACATTCATTTCTCAGTTGAAAGAGAGAAAATTTGAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCCACTCAAAATATGTCAACTNNNNNNNT AGGCCCTTCATAAAACCAAACTG/CJTAGCAAGATGCAAATGCATGGCAAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92 T C ---	---	CTTGATTACTCCACTGAGGTGGGAGCATCTCCAGTGCTCCCCAATTATATCTOCCCACTCCACTAC TCTCTCCCTCCACTTCATTTTCCT/CJTGTGCTCTCTCTCTAATTCAGTGTTTGGAGGCCTGACTTG GGGACAAAGTATATTGATATATTGCTGTTTCTCTCTCCCAATAGAAGAATAAGTCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133 A G ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTG A/GJCGGTAGTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301e	94 T G ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTG/CJTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA TGACGGTAGTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301d	138 A G ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTJA/GJTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301c	211 A C ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC/CJCATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301b	182 C T ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTAC/CJTAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7301	88 G T ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGG/CJTGGGTGGAGGATATGATGTTACAATGAAGGAGGAAATTTTGA TGACGGTAGTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG



WI-7338b	125 A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTTCTTCTTTACACACATATACACACAGACATCAGAAAATTCGTGTT
WI-7338	125 A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTTCTTCTTTACACACATATACACACAGACATCAGAAAATTCGTGTT
WI-7338	221 A G ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTTCTTTACACAC[A/G]TATACACACAGACATCAGAAAATTCGTGTT
WI-7384c	146 T A ---	---	CCTATGTCATGAATGCTAGGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATGATTTTCAATTTGTTGAAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAATTCCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCATGAATGCTAGGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATGATTTTCAATTTGTTGAAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAATTCCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384	145 T A ---	---	CCTATGTCATGAATGCTAGGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATGATTTTCAATTTGTTGAAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAATTCCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7388c	106 A T ---	---	TGAAATCCTGGGTCCTTGGCCTGCTGAGTGTTATTTTACTTTGCCCTCCACCTTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGCTGTCTCCAGAACCTTTTCCCCAAAGATGTTATGTTG
WI-7388b	106 A T ---	---	TGAAATCCTGGGTCCTTGGCCTGCTGAGTGTTATTTTACTTTGCCCTCCACCTTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/T]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGCTGTCTCCAGAACCTTTTCCCCAAAGATGTTATGTTG

WI-7388	94 T A ---	---	TGAATCCTGGGTCTCTGGCCTGCTGCTAGCTGGTTATTTTACTTTTGGCCCTCCCCACCTTTT TGAGATCCATCCTTTTATCAAGAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCACTTATAAAGCATTGCAACAAGTTACCTCTATTTTGGCACAAGGCTCGGGATTGTGTTGA CTTGCTGTGTCGAAGAATTTTCCCCCAAGATGIGTATAGTATTGG
WI-7438	64 A G ---	---	TTAGATTTTAATTGGCAACCAGCAACTCACTGCCACCATCCACTGCAGATCTNCTATTCCTGGIAGI GTTGATATGACAAGGAACCCCTATTGGAACCAAGTCTTCAGATTGNCATGTGCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTACTGTAAACATAGTTTGCTGCTGTTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152 T C ---	---	CCATGATCCCCTCCTCTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAAACCCCTGATAGCACTGTCTGAATGGCAGGAGCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7454	152 T C ---	---	CCATGATCCCCTCCTCTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAAACCCCTGATAGCACTGTCTGAATGGCAGGAGCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7464c	177 G C ---	---	AATTTGAAAATCTGAAAAAAGTGCAATAGCAGAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTAAATTTCCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAGCAGTTGCCA/G/CJCCAGAGAGGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTACCAACAATTAT
WI-7464b	168 C A ---	---	AATTTGAAAATCTGAAAAAAGTGCAATAGCAGAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTAAATTTCCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAGC/AJAGTTGCCAGCCAGAGAGGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTACCAACAATTAT
WI-7464a	103 C A ---	---	AATTTGAAAATCTGAAAAAAGTGCAATAGCAGAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTAAATTTCCCTAT GTACAACAGAGCCACAGCACAGAGGGTGGGCATAGCAGTTGCCAGCCAGAGAGGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTACCAACAATTAT
WI-7499b	134 T T G ---	---	CAATTTCTCAATCCAACTAGTCTGTGCTTAAACCATTCAGACAACTTCCACTTCGAAGGTTTTTA AATGCAATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTTCTTTGAATGCTTCAT /GJTATAGTCCTCTTCAATTTAGCAATCAGTGAGGCAATACACTGGCATCATCCCTTTTTTAGGA ACTCTGTACAAAAATCCCTTTTGAAAAATATAAATTTTGGAAATGAGTGATGA

WI-7499a	33 A G ---			CAATTCTCAATCCAACCTAGTCTGNTGCTTAA/GJCCATTCCAGACAACTCCACTTGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGGACACATCACGTTCTTTGAATGCTTC ATTATAGTCCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGAA CTCTGTACAAAAATCCCTTTGAAAATATAAAATTTTGGAATGAGTGATGA
WI-7506b	118 A C ---			TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAGAGTAGTCTGGTCTGATTGCCCTAGC/CJGGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAATATTTAAAATATTGGACCACCTTGTTCTACCATCCCTACCCACT
WI-7506	118 A C ---			TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCCAGCAGCAGACCACTTNAAGAGTAGTCTGGTCTGATTGCCCTAGC/CJGGAGAGTTGAG TGCCACAGGTAAGAAATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAATATTTAAAATATTGGACCACCTTGTTCTACCATCCCTACCCACT
WI-7534b	143 C T ---			TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGGTTCTTGATGTGTGCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCGGGTGATAGAAATGCT AAATTGTC/JGGTGAATAGGTTAGAAATTTTCTTAAATATGTTTTCTTATTCTGTGAAAAATTCGG AGAGTGTCTGCTAAAATGGATGGTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---			TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGGTTCTTGATGTGTGCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCGGGTGATAGAAATGCT /CJAAATTTGTCGTGAATAGGTTAGAAATTTTCTTAAATATGTTTTCTTATTCTGTGAAAAATTCGG AGAGTGTCTGCTAAAATGGATGGTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---			GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCACTTGAAGGAAGAAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTTCCTTGAAGAACCACTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---			GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCACTTGAAGGAAGAAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTTCCTTGAAGAACCACTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---			GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGT/CJCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCTGATTCCTGTTAAAGCCACTTGGGT ATAAGAGGGAAGTAAAAAATGAAGTCTGACTAGAAATTTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATGAGTTGTGATATAGTTTTCATTTGATGTCATTTTGAATTCAG





WI-7577j	117 A G ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTGAGGGTTTTAGTA[G/C]ACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577i	77 T C ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTGAGGGTTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50 G C ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTGAGGGTTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157 G A ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTGAGGGTTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48 A G ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTGAGGGTTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84 G A ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTGAGGGTTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93 T C ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTGAGGGTTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154 C A ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTGAGGGTTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC



WI-7577b	117	A G ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAGGTTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTAATATGGGCTGTTATACATGACACTCTTCTGAATTGACTGATTTTC
WI-7577	107	G A ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAG/GJGTTTTAGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGTAATATGGGCTGTTATACATGACACTCTTCTGAATTGACTGATTTTC
WI-7619q	106	C G ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCACAAGAC AGAGAAAGGGCCAAATGGGGTCAATCCCTCCCTAACGAGACTTC/GTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150	T C ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCACAAGAC AGAGAAAGGGCCAAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228	A G ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCACAAGAC AGAGAAAGGGCCAAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTCCTC CGCTTTCTTTCTTACACAGAAACATAG/CACATACCGAGAAACCTATTTC
WI-7619n	237	G C ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCACAAGAC AGAGAAAGGGCCAAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTCCTC CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99	C T ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCACAAGAC AGAGAAAGGGCCAAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG TGGCAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189	T A ---	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCACAAGAC AGAGAAAGGGCCAAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTGGGCTGTCTCTCCCTTTTCCATCTTTTCCCTCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCG/C/GCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	106 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCAATCC[C]GCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT CGCTT/GTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGC[G]GTTAAACCATCATGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTC
WI-7626c	155 C T ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATGACCAAAATGTGCCA TACTAATGATGAGCAATTTAG[C]TJACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTC
WI-7626b	28 T A ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAG TAATCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTC
WI-7626	144 T C ---	---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATGACCAAAATGTGCCA TACTAATGATGAGCAATTTAGCACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCATTTTCCCTTGGACTGTTC
WI-7689c	134 A G ---	---	---	TCCCAACCCGCTGATCTCAGGGTCTCTGCTGCCGCCCAACCAAGATGGGGAAAGCAGAGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTTAAAJA /GJTAAGGGCAGAGTCACACTGGGCGAGCTGATACAAATTCAGACTGTGTAAAGAGAGGCTTAAT GATAATATTGGTGGCCACAAATAAAATGGATTATTAGAAATTCATATGAC

WI-7689b	134	A G ---				TCCCATAACCGCTGATTCACAGGCTCTGCTGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGAAAGGTGTTCTCTAAAG /GTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAAATGGATTTATTAGAATTCATATGAC
WI-7689	121	G A ---				TCCCATAACCGCTGATTCACAGGCTCTGCTGCCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGAAAGGTGTTCTCTAA AATAAGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAAATGGATTTATTAGAATTCATATGAC
WI-7690	45	G A ---				TGGAGAACATTCATCTGCCGTCACTATTCAATCAATGAAGATTG/AJCACTGAGATCCAGAGAGG CTGGATGACTTGTCAAGTTCAACAGCATGGTAGTGCAAGAGAGGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTCCCAAAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGCCACCCAGGAAGCAC AGGTCAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTCAATCC
WI-7703b	164	T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTACATTTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGTCATAAACCAAACTGATGTAAGTAAATTCJGGTCTCTCACTGTTTTATTAACTCTAAATTCCT TTCATTTTAGGGTAGCATTTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7703	156	T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTACATTTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGTCATAAACCAAACTGATGTCJAGTAAATGGTCTCTCACTGTTTTATTAACTCTAAATTCCT TTCATTTTAGGGTAGCATTTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---				TTAAATGAGTGTGTTGTACCCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCCTTGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCCTATCCGAGGAGGTCAGGAGAG GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC
WI-7743d	275	C T ---				TTAAATGAGTGTGTTGTACCCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCCTTGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCCTATCCGAGGAGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC
WI-7743e	106	C A ---				TTAAATGAGTGTGTTGTACCCGTTGGGATTTGGGAAGACTGTGGCTGCTGGCCTTGAGCCAAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCCTATCCGAGGAGGTCAGGAGAG GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC

WI-7743d	275 C T	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTGGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743e	106 C A	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTGGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAGAG GGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743d	275 C T	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTGGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743c	106 C A	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTGGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAGAG GGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743b	275 C T	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTGGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	106 C A	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTGGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAGAG GGGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7743	275 C T	---	---	TTAAATGAGTGTGTTGTACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTACTGGGTCTGGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAACG
WI-7758	144 A G	---	---	TGACATTATTCAAAGTTAAAGCAACACTTACAGAAATTATGAAGAGGTATCTGTTTAACTTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC[A/G]TAGTTTAACTGCATTATAAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAAATGTGTAATTTGTTTATATTTCCTATTTCCCAATTTGGACTGTAACTGACTGCC

WI-7765b	126	G C	---			ACAGGGCCCTTTGGCAGGTGCAGCCCCACCTGCTTTGACCTGCTCCCTTCATGCATGGAATTCCTCTCATCTGGAAACATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TTAGGGAACATTCCTCCTTGAGTCAAAAAATCTCAATCTCTCCCTATCTTTGCCACCCCTCATGCTGTGTGACTCAAACCAAAATCACTGAACCTTTGCTGAGCCCTGTAATAAAAGGTCGGA
WI-7773b	237	C G	---			TTAATTTACTGATCCAGCAAGACCAATCAATGTATCAGATTATTTTAAGTTTTATCCGTAGTTTTGATAAAAGATTTCTCTATTCCTGTTCTGTCAGAGAACCTAATAAGTCTACTTTGCCATTAAAGGCA GACTAGGGTTCATGCTCTTTTACCCTTTNNNNNNNNNTGTAAGTCTAGTTACCTACTCTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAAC[G/C]TTTCGACGTTTGA
WI-7774b	170	T C	---			TGCAACCTCTTTTCGTGATGGGAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGACGGCACCCAGAATCAGATCCCAGCTTCGGCATTTGATCAGACCAACAGTCTGTTTCCCGGGAGGAAACACTTTTITTAATTACCTTTTCAGGACCACTTTAATCTGTTT[C/G]ATACCTTGTCTTATTAAATGAGCGACTTAAATGATTGAAAATAATGCTGCTCTTTAGTAGCAAGTAAATGTGCTTTGCT
WI-7785c	165	G	---			GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGATTAGAAATA TTTATTGCTGTAAATCTGTAATGCAATGGAAATAAACTGTCTCCCCATTTGCTCTATGAAACTGCACATTGGTCATTGTAATANNNNNNNNNNNGCCAAAGGTAATCCAATTATTATCACAATTTACCA TAATTTATTTTGCCATTGATGATTTATTTTGTAATGTATCTTGGTGCTGC
WI-7785b	165	G	---			GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGATTAGAAATA TTTATTGCTGTAAATCTGTAATGCAATGGAAATAAACTGTCTCCCCATTTGCTCTATGAAACTGCACATTGGTCATTGTAATANNNNNNNNNNNGCCAAAGGTAATCCAATTATTATCACAATTTACCA TAATTTATTTTGCCATTGATGATTTATTTTGTAATGTATCTTGGTGCTGC
WI-7785	156	T	---			GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGATTAGAAATA TTTATTGCTGTAAATCTGTAATGCAATGGAAATAAACTGTCTCCCCATTTGCTCTATGAAACTGCACATTGGTCATTGTAATANNN- /TJNNNNNNNGCCAAAGGCTAATCCAATTATTATTATCACAATTTACCATAATTTATTTTGTCATTGATGATTTATTGTAATGTATCTTGGTG
WI-7789c	84	G A	---			TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTAATGAAGCTAATGTGAATGTGAAGTCCCTTCAAGCCCGCTGCGCTAGGATAT GGCCTCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84	G A	---			TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTAATGAAGCTAATGTGAATGTGAAGTCCCTTCAAGCCCGCTGCGCTAGGATAT GGCCTCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT

WI-7789	73 G A ---	---	---	<p>             TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGCGACCACATCTTACAGAGACTCTCCG              TGACG[G/A]TGGAAATTTAAGTTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC              CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT              GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCCATCT           </p>
WI-7790b	190 C T ---	---	---	<p>             AATTGTGAGTCACCTCTTCAAAACCTTACAGTCCTTCTTAAGTTACTCTTCATGAGATTCATCCATT              TACTAATACTGTATTTTGGTGGACTAGGCTTGCTATGTGCTTATGTGTAGCTTTTACTTTTATGG              TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[C/TT]TCTATACITTT              AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACITTAAC           </p>
WI-7790	190 C T ---	---	---	<p>             AATTGTGAGTCACCTCTTCAAAACCTTACAGTCCTTCTTAAGTTACTCTTCATGAGATTCATCCATT              TACTAATACTGTATTTTGGTGGACTAGGCTTGCTATGTGCTTATGTGTAGCTTTTACTTTTATGG              TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[C/TT]TCTATACITTT              AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACITTAAC           </p>
WI-7795b	81 C A ---	---	---	<p>             CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCCTTGGCTCATATTTCTTTCTTCAT              CTTGATGATGAT[C/A]GTGATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT              TAATAAGCCACATATAAATGTACTTTTCTCCAGAAAATCTCCTTGAGGAAAATGTCCAAAA              TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAAATAAATCTG           </p>
WI-7795	81 C A ---	---	---	<p>             CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCCTTGGCTCATATTTCTTTCTTCAT              CTTGATGATGAT[C/A]GTGATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT              TAATAAGCCACATATAAATGTACTTTTCTCCAGAAAATCTCCTTGAGGAAAATGTCCAAAA              TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAAATAAATCTG           </p>
WI-7814c	41 G A ---	---	---	<p>             TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACCTC              TGTCTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC              ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAAATAATGGGATTTTC              TTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA           </p>
WI-7814b	41 G A ---	---	---	<p>             TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACCTC              TGTCTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC              ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAAATAATGGGATTTTC              TTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA           </p>
WI-7814	28 G A ---	---	---	<p>             TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACCTC              TGTCTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC              ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTAGGATAAAAAATAATGGGATTTTC              TTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA           </p>

WI-7830d	150	C T	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTATCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C]/TTAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTTCCCTTTG AGGTTGATCGTTGTTGTTTGTGCTGCACITTTTACTTTTTGCGTGTGGA
WI-7830c	54	G A	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTATCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTTCCCTTTG AGGTTGATCGTTGTTGTTTGTGCTGCACITTTTACTTTTTGCGTGTGGA
WI-7830b	134	G A	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTATCATCACATTTCTATGCCAAACAGGAAC G/AJATCCATAACTTTAGTCTTAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTTCCCTTTG AGGTTGATCGTTGTTGTTTGTGCTGCACITTTTACTTTTTGCGTGTGGA
WI-7830	44	A G	---			GCAGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGT[A]/GAGAAGTCTGTCTGTCTGA TGATGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTATCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTTCCCTTTG AGGTTGATCGTTGTTGTTTGTGCTGCACITTTTACTTTTTGCGTGTGGA
WI-7865e	25	C T	---			CCACTTCTCTATCTGATTTTCCCAG[C]/TAAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAGATTTAGGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191	C T	---			CCACTTCTCTATCTGATTTTCCCAG[C]/TAAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG ATGCTACTCATAGATTTAGGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGT[C]/TGA AAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25	C T	---			CCACTTCTCTATCTGATTTTCCCAG[C]/TAAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAGATTTAGGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191	C T	---			CCACTTCTCTATCTGATTTTCCCAGCAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAGATTTAGGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGT[C]/TGA AAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA



WI-7865	25 C T ---	---	CCACTTCCTATCTGATTTTCCACAG[C]/AAATGAGGCAGGCAATTCTAGTCTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTACATAAGATTTCAAGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCTATGTAAGGAAAGTGCTATTACCCAGTAACCCAAA
WI-7865	191 C T ---	---	CCACTTCCTATCTGATTTTCCACAGAAATGAGGCAGGCAATTTAGTCTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTCAAGGTGCTTCCAACTGAAATCTCAATGTTCTCAGT[C]/TGA AAAAC CTGAAATCACATGCTATGTAAGGAAAGTGCTATTACCCAGTAACCCAAA
WI-7867c	92 A C ---	---	TTCAAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACTTCCAGCTCAGCTCAGTCCCC CTAACAAATTACCTGTCAAGAGG[C]/GAGTGCAGCTCAGGTGGATTTAATGTGGTTTAAATATGGC CTGTTGAGTTTAAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C ---	---	TTCAAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACTTCCAGCTCAGCTCAGTCCCC CTAACAAATTACCTGTCAAGAGG[C]/GAGTGCAGCTCAGGTGGATTTAATGTGGTTTAAATATGGC CTGTTGAGTTTAAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T ---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CACCCAACTGTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA[C]/TTAGAGGCCAGAAAAATGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTTCAATTAATGCCTAGAT
WI-7868b	173 C T ---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT /CTCACCCAACTGTCCCTCTGATCCTCCATCAGGGCCAGATCTTCCACGTCTCCATCTCAGTACAC AATCATTTAATATTTCCCTGTCTTACCCCTATTCAAGCACTAGAGGCCAGAAAAATGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTTCAATTAATGCCTAGAT
WI-7868	66 T C ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGGTGGCGGGAATCC[C]/AATTTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATGCTGCAAAAATGAAATCCAAATGAGCACTAGAAATTTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGAGACCACCTAATATCAATTG
WI-7870b	85 T C ---	---	

WI-7870	76 C T ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGGTG[C/][GGGAATCCTATTATCAGACTCTGTAATGAATATAAATGTTTTACTCAGAGGAG CTGCAAAATGGCTGCAAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATTTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C ---	---	---	TTAGGTCTATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGGAAGTCACTACAGGACTGGCCGGGCCAGGGCCTCT GGCTCCCTGCCAATCCTCCCTGGAGAGGGACATGGGAATGAATTTGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGCTGCTCTCCAGAGCACAAAG
WI-7889b	54 C ---	---	---	TTAGGTCTATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGGAAGTCACTACAGGACTGGCCGGGCCAGGGCCTCT GGCTCCCTGCCAATCCTCCCTGGAGAGGGACATGGGAATGAATTTGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGCTGCTCTCCAGAGCACAAAG
WI-7894c	142 A G ---	---	---	AGCCACCCCCAAATATAACTGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTTGTGAATTTATTTGCGTATAC ATTATC[A/G]TATGTAAATTTGCAATTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	---	AGCCACCCCCAAATATAACTGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATTGTTTGTGAATTTATTTGCGTATAC ATTATC[A/G]TATGTAAATTTGCAATTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/][CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/][CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/][CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC

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WI-7901	33 C T ---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATAC/TJAGACACACACAGGACACATATATTAAACAG ATTGTTTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAACTCCAGCCCTTGGTTGGGTCGCTGGTTATGGGCGAGCGCGTGGTGGT CACTCAGTCGCTCGCATGCTCTCTGTCATACAGACAGGTAACTAGTCT
WI-7901	271 T G ---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAAACAGATT GTTTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGACCCCT TTTAAACAACTCCAGCCCTTGGTTGGGTCGCTGGTTATGGGCGAGCGCGTGGTGGTGCAC TCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACTAGTCTGTGT
WI-7926c	150 C A ---	---	---	CATTCCGCATCTGTCAACAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAGCAAAGTGATACAAACACAGTATTTGGGAATGCCCTTCATT TACAATGCAATACCTA/C/AJATTTTAACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28 A T ---	---	---	CATTCCGCATCTGTCAACAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCAC ACTTTGGAGATCAGAAAATTCATATTTAGCAAAGTGATACAAACACAGTATTTGGGAATGCCCTTC ATTACAATGCAATACCTA/C/AJATTTTAACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150 C A ---	---	---	CATTCCGCATCTGTCAACAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAGCAAAGTGATACAAACACAGTATTTGGGAATGCCCTTCATT TACAATGCAATACCTA/C/AJATTTTAACTCTTGAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203 G T ---	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACCAATAGCAGCCAGCCACAGGCCAGGTCCTGT GCTATCACAGGTCACCTCTTTACAGTTAGAAACACCCAGCCAGGCCACAGATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTGGAAGCCACA GA/G/TJCTCTCCCTGGAGCAGCAGACTATGGGAGCCCGAGTCTGCCACCTG
WI-7947	203 G T ---	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACCAATAGCAGCCAGCCACAGGCCAGGTCCTGT GCTATCACAGGTCACCTCTTTACAGTTAGAAACACCCAGCCAGGCCACAGATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTGGAAGCCACA GA/G/TJCTCTCCCTGGAGCAGCAGACTATGGGAGCCCGAGTCTGCCACCTG
WI-7963b	145 T C ---	---	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAAGTAAGACTAATTTTAAAAATAAAAAATGCC ACAAATTTTCATTTCTCCCTCTAAGTATTACAATGGAGTTTATCTCGCCTAAAAAGTGGAAGAAAT TGAGTGAATGA/TJCAATTTTGTAAATTTAGGATAAGATCCCAAGTTATTTCCCCAACTCTTGTTCCTC CCATAAAGTTAGGCATGAGGAGGAGCACTCATTTAAAGGCAGAAAGACGGGAAAA

[illegible]

WI-8021b	57	C T ---	---	---	ACAACTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAA[C/T]GATCCC ACGTCCTTAGAACCTTACCACAGAGTTTCTTGTAGTGATCTCAAGTCTTGGTAGGCATTCCGA ACTGGTCCTTTCACITTTGAGATCTTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8021	57	C T ---	---	---	ACAATCTCAGAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAA[C/T]GATCCC ACGTCCTTAGAACCTTACCACAGAGTTTCTTGTAGTGATCTCAAGTCTTGGTAGGCATTCCGA ACTGGTCCTTTCACITTTGAGATCTTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8024c	206	A G ---	---	---	CTGAAATTTACTATGCTCTCCACAAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTCTATCACCACAAACCATTTTCAGCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTCAGTACACAAAGGAAAGAGC
WI-8024b	206	A G ---	---	---	CTGAAATTTACTATGCTCTCCACAAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTCTATCACCACAAACCATTTTCAGCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTCAGTACACAAAGGAAAGAGC
WI-8077	167	A G ---	---	---	GAATGAGCCTTCTAGCGCCGAGGGACCTGCTGCTGTTGTCCTGCACATGCATTCATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTCGCCCAAACCTCCTTCT AAGGAGCTGGGGTGTATGCCCTACAAAC[C/A/G]TAAATTCATCAGATGGATTTTATTTAAGCTT GTGATTTGAGACTTACTTTCCAAATCTGACTCTGGCATAACAAGGGAAAAA
WI-8118f	114	G C ---	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAAATGAGCTTGT[G/C]TTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G ---	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAAATGAGCTTGT[G/C]TTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G ---	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAAATGAGCTTGT[G/C]TTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTTAAATCAAAAGCAATTTGCANITTTGGATTTTGGAAATGA/C/TCACTCCCTTGCTAAGGAAGC TATGTAATTCATGCTGTGGAACTGGCAATACAGAATGAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTTCGATTTCCCTGCTCCTCTATTCCTTCCT AAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTAAATCAAAAGCAATTTGCANITTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAAC/T/CIGGCAATACAGAATGAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTTCGATTTCCCTGCTCCTCTATTCCTTCCT AAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCACACA TTTATGGAGGGTTGTCCTGAAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACIA/GTGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGGTTGTCCTGAAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACIAG/TGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGGTTGTCCTGAAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCACACA TTTATGGAGGGTTGTCCTGAAGAGAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGGCCATTGCAATTTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGGI/GC/AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCAGCTGTCCAATAGAATTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCACT
WI-8314	78 C/G ---			GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGGCCATTGCAATTTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCAGCTGTCCAATAGAATTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCACT

WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTTATACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATTCTTTCTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTTATACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATTCTTTCTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8332b	123	A C ---	---	TATGACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTTTTCCCTTCCCTGTGCAGCCTTAGA/JCJACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C ---	---	TATGACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTTTTCCCTTCCCTGTGCJAJGCTTAGAAACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGGAGAAAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACTNTCACCAGGCCCTCCTCCACACAGTGTTGGG
WI-8378	308	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGGAGAAAGTCTACACACTTTT AAACAACCCAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACTNTCACCAGGCCCTCCTCCACACAGTGTTGGG
WI-8426	184	T G ---	---	TTTAGCACATATTTAGCATTAAAGCCTCAAACGATACAGCAATATGTTACATTCTCTGTGAAAAACAG TTGTTGTAGACTGTTAANNNNNNNNAATGTAACCTCGACCTGTGCCCTAATAGGATTTGACCNITAA GAGGNTTCTTTGCTGTGGANGGGGTGGCTTGTCTGAACTTCCATTCTGT/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGGNCOCGGGGCOCTTGGGNATNGNATTCAGTGAG
WI-8450b	61	C A ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTTC/AJCA TCTTCTATCTTAGTCCAAAGTTTGTGTTTCAATCCCAATATACCAATTCATGTTATTTTAAAGA AAAAACCTTCCCAGTTATGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGICTTAATGCAATTCAT



WI-8450g	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G ---			CAAGGAAGCTGTCAGTCTTCAAACTTTCAAGAGTTACAAAAATACGTAATTTTTTAAAGJCTA CAATTCAGATTAGCATCCAAACCTACAAACATGATGATACATTCGTACACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATAGTTTGTGAAACCTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---				CTTCCTCCTCCAAAAATCTACATGAATACCTTGAAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTTAA/NNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAATTTTACAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---				CTTCCTCCTCCAAAAATCTACATGAATACCTTGAAGACAAT/CJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATCAATTTTNNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAATTTTACAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---				CTTCCTCCTCCAAAAATCTACATGAATACCTTGAAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTTAA/NNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAATTTTACAANTTTNTTGAAGAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---				AATAACATGTTATGAAACAAGCTGTTACAAGTAGTAGGTAGTGACTTAATTTTGATAAAAAAAT TAAAAAGCATTA/GJAACATGCATATAAAAAATTAGATTATGTACAAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATAATTCCTCCCTTTGTTTGTCTTTTAAAAAACATTAATTTCTGAAAAAATAA ATCAGAAAAACATGATCGTGGAGAGAAATTA
WI-9438	77 A G ---				ACAGAAATGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAATCCAGTCTGTCAGCTCAGTACCTGT[C/T]GTGACACTGTACCATCTCAGTCCCAGTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCAAGAGGCTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTGTCTGAGCTAGAAAACTTGACCTGTAAAAACAAG
WI-9439b	101 C T ---				ACAGAAATGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAAAT/C/CCAGTCTGTCAGCTCAGTACCTGTCTGTGACACTGTACCATCTCAGTCCCAGTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCAAGAGGCTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTGTCTGAGCTAGAAAACTTGACCTGTAAAAACAAG
WI-9439a	76 C T ---				GAAGGCTTGATTAGGGAGGNTTTATTTGATGTGNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT/C/CJCCCTAAAGNGACACATGCCCCAAATGACCANGNCATAGCAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGTGNNCCCTACINTTATCACTGTGTCTTCTGTTTGTGTACCTA TGNGAACTGCACACTAICTGTGGCAATATGT
WI-9446b	75 T C ---				

WI-9446	75	T C	---	GAAGGCTTGATTAAAGGGAGGNTTTATTTGATGTNAACCTACCATTCOCATAGACTATAAAGANCATTA TAAAAAAAT/CJCCCTCTAAAGNGACACATGCCCAAATGACCCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTTGNCCCTTACCTTTATATCACTGTGCTCTCTGCTCTTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACATTTT GAGATAATTATCTAGATTCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCITTAATTAATCAAAGTATGTTAATGTCACCT GGAATTTCTACATGGAAAAGCCCAACAAATAACTAAAACTTGACTAATGAAG
WI-9497	185	A	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAATGGTATATATACATTTT GAGATAATTATCTAGATTCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCITTAATTAATCAAAGTATGTTAATGTCACCT GGAATTTCTACATGGAAAAGCCCAACAAATAACTAAAACTTGACTAATGAAG
WI-9523b	193	C A	---	GTGAAAAAGTTTCTATTTCATCCATCATACATAGATTTGCTAAGGATCATTTTGGAGAATGTG CAGCATTCAGAAAGTTGATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTAGCCCATGATCTATGGTATTTCCACACATTTGTA/C/AJAGTG AAAGCTTTCAGCTTGGAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G A	---	GTGAAAAAGTTTCTATTTCATCCATCATACAAATAGATTGTGCTAAG/G/AJATCATTTTGGAGAAT GTGAGCATTCAGAAAGTTGATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTAGCCCATGATCTATGGTATTTCCACACATTTGTACAGTGA AAGCTCTTCAGCTTGGAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9554	202	T C	---	AAAAACACAAGTTTTCATACATCACAAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGATAGTACTGCCCTTTCAGTTTGTATTGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTCTACACCCCAAGTACAATATGATAAAGCAGCCCTCTGTCAAGTG GT/C/GCTGGATACCACTAAGAAAGTCTACTGCAGCCCATGTTGGTTATGATTTT
WI-9555	97	G A	---	CCAAAGCCAAACCATTTCATATGATGGATTTCATAAACAATTTATGATCCTTTTGGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/G/AJCTTGAAAAATCAATTTCAAGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAAGGCACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAAGGCTGTAACTCTTTTNCCTCACAATTGATCACA
WI-9625b	172	A/T	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAAATCTGCAAGTAAATCAATCATTTT TAAACATAGCTACCATATATTTGTATCTNCCTCTGGGAAAAAATTTGGAAAAAATAACACGCACA TAAGTATCATAACTGAGGGTTGGGACAAGTTACTCTG/AJGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTNCTCCTGGGAAAAACCTTTGGAAAAAAACACGCACA TAAGTATCATAAAGTGGGTTGGACAAGTTACTTCT[AT]GTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTTCAATTAATAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---			TTTTCTGAGATCAAGAGCTACATTTTGGTAGTGATGTCTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAAGCT TACAACTTC[AT]GTCTTTACCTGATACATTTATCCATTTACTTTTCAATTTTGAATTTTAAAAATGTTA ACTTAATACGTCCTTTTCAGATGTCCTGCTTTTGTAGTTAATGTGTTT
WI-9676n	114 A G ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCA[AG]GATGTGGCTTTCTGCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTGTTT
WI-9676m	184 G T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGC[GT]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTGTTT
WI-9676l	84 A C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTGTTT
WI-9676k	202 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA[GT] C[TT]CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTGTTT
WI-9676j	92 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTGTTT
WI-9676i	173 T C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTT[CT]CCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTGTTT

WI-9676h	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTCGCCCG C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTCGCCCG ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTCGCCCG ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTCGCCCG ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTCGCCCG CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTCGCCCG CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTCGCCCG CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCTCGCCCG CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9738b	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGGCCTGTGTA[C/A]ATTACAACATCATGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATAAGTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGTTTTCACATATGTGAGTATCTA TCCTTTTATTTCTGCTCCCTATGTTGGTGGC/CACATGCTGTATTGCTGTCC
WI-9738	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGGCCTGTGTA[C/A]ATTACAACATCATGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAATAAGTCCACATTTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGTTTTCACATATGTGAGTATCTA TCCTTTTATTTCTGCTCCCTATGTTGGTGGC/CACATGCTGTATTGCTGTCC
WI-9756	47	A ---	---	ACTGAAATGTAATGGCCAAAGGCCACCCAGGACCTTAAAAATCATAAGAAAGTTAATCTGTGGAAAA GAGTAACTACAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGTCCTTATCACATTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTTCCACAAACACACAGAAATATACACATTTTGGGAG ATTCCACTTAACCACTTGATCTTCACCTTTTATGATTTAAAACTCTCCGTGG
WI-9758	135	A G ---	---	GATGGTCCCTTAAGGATTTGCAATTGTTAATGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAAACTGGGAGAAATCAATCAAAGAAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A/A/GTAAAAAATAACTCTGTGAGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGGTTTCTAAAT ATTACG
WI-9778	127	G A ---	---	ATTTAAATCCAGGCAGCGGGGAAATGGATACATTTTCATATGCTCTGTACCCCAACTATAAACTTTTG GTTCTCATGCAACCATTTTCATTTTGCTTCTCACTCCAAAGTACCACATGATTTTACCAATT[G/A]CTCTC ATAATTGACTTTGCTACTGGAAGAAACTCTTAGAATGTTGGAATTTCTCTATTACACACATTTTGCCTCA AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A ---	---	TCCTCCCTTTGCTCTCATGCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGCTGACAAATGCAGTTT[C/A]TGGATCCACCCAGGA CTCAAAAATACTAGGAATTGGGAGAAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAAGTGGACTAAAGTTGAGGACCCAGACATGGAAGTTGGCTTTGGC
WI-9841	101	A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAATGGCATGA TATGAAATTCCTATTTTGAATGAATAAAATATAC[A/G]TGTGTATGTATATATACTATTAAACACTT AGGATTATATACACACAATAAAACGCTGTGAAGGATAAACTAAGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTGTTACTTTGATATGCTGTG
WI-9880c	222	G A ---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCCAAGGGAGGCTGTGA GTTGTTTTCTACATCCCTTGGACTATAAAGATCCCTCTTTTAAATATATTTTATAAGCACATGAA AATGGAATGAAATAATGA[G/A]TTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A ---	---	GAAC TAAC ACC TTT CTG CAT GGAT TTT CTG ATT ATGG CAG TTAACA ATAAAT GTTATT AGATC ACTGGT GCTTCTGTG TGGGTTGAG TTTT TATG ATATCTCTG TTAGAC CCAATAAGGGAGGCTGTGA GTTG TTTTCTACATCC TTTGGA[C/A]TATATAAGATCC TCTTTTAAAATTATATTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ---	---	GAACTAACACCTTTCTTGCATGGATTTTCTTGATTATGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTTCTGTG TGGGTTGAG TTTT TATG ATATCTCTG TTAGAC CCAATAAGGGAGGCTG TGAGTTGTTTCTACATCC TTTGGA[C/A]TATATAAGATCC TCTTTTAAAATTATATTTATATAAGCACAT GAAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ---	---	ACACTGCAGGCACCTCCAAATCCTNACAGACATATGCACTTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAAAACAACGCCCCAGTTATCACAGTTTCTNTTTTGT[C/T]CACC ATTTTCCATAACAAAAAGAGCTACACAAAATTNGGGGGAGANACTCTCTTTGGAGACTGCACACATT TGCAGAGGGGTCAATGAATAATGATTCCAAA
FB25G10b	109	A G ---	---	TCCCTCAATGACAGATGAAC TAAATTTTCTCTTGGGTAAGAAATAC TTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAAC TGAACCTATTTATACATAAAATGGAATGTAAGAACC TATTTTGGATATCC GGAC
FB25G10	109	A G ---	---	TCCCTCAATGACAGATGAAC TAAATTTTCTCTTGGGTAAGAAATAC TTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAATGGA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAAC TGAACCTATTTATACATAAAATGGAATGTAAGAACC TATTTTGGATATCC GGAC
IB3071	102	C A ---	---	ACAACGCTGAAC TTTCCATAACAGTCAATGGTACAGTCAAAACATCACA TGTACAGAACACACAATTTA GATGAACTGAAATTAAGNTAAATAAAATAAAAT[C/A]CAATTTTCAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATCTTAAACCCTAATGAGATTTCACTGNGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCCTATTAAACCCAGTCTAGGGATTCTG
NIB551	161	C T ---	---	CGTCC TTTCC TTTT GAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTGGGTTGTCCC TACTGAGCTTGGGGCCAGGTGTGTACTTAGGAACCCCAATCCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C/T]TGACACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAGCTTGTC
S72904	51	G T ---	---	AGCATAGAAAAGTGATTTATATTTTAAATGGTTTCAAGTGGAAAGTTCCTTT[G/T]AATTTGTCAGTTC ATTCTGGAAAATCTTTTGAGTTAAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAAATGCCTCAAACCAAGTGCTGAAC TCTCCCTCTTCTGTCAATTGGTTGTTCTTTAAATA TTGCAAAAGTCCCTGATGCTAAACAGTATTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTGGTTAAAGACTGAATTTGTAAACC CATTCAGATAAATGGCAGTACTTTAGGACACACACAAACACACAGAC/C/TACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCTTCACANTCAATACTGTGGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCCTCACANGCTGTATTACCTTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23	---	---	---	AACTCTCACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTCCTTTAAATGTAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCCACATGATACNTAAGTTCAAGGTCCAAGTTCCTATCACAAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTT
ESTC122	34	---	---	---	GACAATAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCAGGCCATCATNTTCCATGGGACCAGGCTGGCTCAA TGTTGAACTGG
ESTC129	20	---	---	---	AGTCACCATGCCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAAATCTTCAGGAAAAATGAACANGAGAAGCTGAAACAAT CTACACCTGAATG



ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAAAACNCTATGTTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTGGCTTCTGTCTCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	---	---	AGGACACAGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGNGGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTGTGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCATTTTAAATC AAAGANACCATTCATTTCCTAACAAACA
ESTC143	29	---	---	---	GTTTACGAAAGTACTGAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTCTTGACATGAGGTNGCTTTTATAGCAGCATTTTCGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGNATGACGGGCTGTGGAGGCCCTG GGGTGGCTGGGCTGTGCTCTGAG
ESTC149	28	---	---	---	TCAGTTCATTATTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAAGTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAAAACAAGCAGACACANACTTATAGAATACCTTGGTTTAAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGGCCCCATTTTTTCTTTTAAATACAAATCTACTGGTGTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACATACAGTNTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCATTTTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGCGCAAAACAAANCCCTGGCTGCTCGGGATGGAGCGGGGGGCTCA CCACCACTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCCCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT TTCTAGCATTGCTGGTGCAGTGGGGCCCTGAGCTGGGNGCAGTCGGCAGTGTCACCTGGGCCCGTTTG GGACTGGGTTGA
ESTC160	38	---	---	---	CTCTCGTCCGTTTGCAAGTTGCTGTTTCCAGNTACACAGTCAGAGCTCCACAG TCATTCTCCATAGAATATTGGTTTTGTAACANCGAATACAATCCAATATATAACATTAAAACAATCC GATACATACCA
ESTC162	36	---	---	---	GTCTCTGGTGCAGGGAATCANITTTGCTGGATTAGAGGAAAGGTGCCGCCGCTCTGTTTCCAIGACTT
ESTC164	31	---	---	---	CACCTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA TGGTGGCTCTTTAAATACCTTCCATTATATTTCAAATTTTNCCTTATTCTATTAAAATACCTTTTAT TCTCTTATCCCATAAAAAGGCAACCAA
ESTC169	22	---	---	---	TCAGACACTGCCGACATCAGCATTGCTCNCNTGTACAGCTCCCTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC176	23	---	---	---	TAGGGATTCCAAGTTGCCCTGGNITTAATATAATACATATTCACAAAAATTTACACAGCTCATGCATAC CA
ESTC177	42	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAGTGCCAGATNAGTGCTAATTGTCAATTCAGCTTG ATTTTCAACCTCA
ESTC18	29	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG TCTATTACAGGGTTATGTCACACCNTGTCAACCTGTCAACCTCAAAACAGATGATCACTCACTTGCTCTCCAT CTTGC
ESTC181	21	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCAGACTCGTGATCA
ESTC186	43	---	---	---	TCCTCAAATACCACTTCCCCTAACTTATCAGTCTAGTAGCNITTTCAAAGGAGGAAAAATGGGTAC CTTTCAGGGG
ESTC187	24	---	---	---	ATCTCCAGTGTCTGCTGCCCTCCTCCNGCAAAAGTCTCCCAACAGCACA
ESTC188	25	---	---	---	AAGATTAGGACAGACCGGTATAGTAGCTCTGNGGAACTCCAAGAACTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC189	27	---	---	---	TTTGGTGAAAAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGGCTGCAACAG
ESTC196	42	---	---	---	
ESTC197	26	---	---	---	
ESTC20	33	---	---	---	
ESTC200	44	---	---	---	

ESTC201	35	---	---	---	---	TCCTACTTGGGTAGTATTAGCAACATTTTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGGAGGGAGGACAGACGNCAGCGGCTGGGTGGCGCCCCCAGAAAGGCTGGCGTGGATGTT CGAGATGAGCC
ESTC203	27	---	---	---	---	ACACTTAACAGGGTTAAAAATATCCAAATNAAATTTACTGCAACTTTTGAGAAATTTTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC CTAAGAGTGAAAA
ESTC210	29	---	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAAGTGAAGTGAACCTGCTG
ESTC212	27	---	---	---	---	GGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	---	CTCAGAGTCCCTCCTCCTCANACCAGGGCAGGAGGATTAGGGAAT
ESTC216	49	---	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTTAAATTTAATCACAGGTATNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	---	TTTTGTCAGTAAATGAGCAATACACTGANTGGAAATCTGCATGATTAAATAACATTAACAAGTTCAT AAACACACCCCA
ESTC219	32	---	---	---	---	GTACACATCCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	---	---	---	---	TCATTGAAGAAATATGGGTTTTTATCTTATTTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGCC
ESTC223	27	---	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTCTTGATTTAAAAAACAGAAAGGGAGGAGGA
ESTC224	37	---	---	---	---	CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACA
ESTC225	20	---	---	---	---	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAAGTCTTCAGAAGGA ATGTGATGATCG
ESTC23	27	---	---	---	---	TTCTACTTTATTTTCATATCCCACCACNATAACGACTCCTTTAATTTAACTAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	---	GCTTCCTCCACGAATTTGAAGACATATTGGCTGACCTGATACINTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	---	CAAAAGGGTAGTCATATTTCCCCANCAACAGCATGATAAAATAATTCAAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTCTTCTCTATTCCTATAAAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTTATCTTGAGCCGCTTGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAACAATATNTCAGTCGGTGATCATTTGTAATATACAATACAAAG CAATTTCTCTCAGA
ESTC33	25	---	---	---	AGCACTCCAGCTCCTTGACGTTGTNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAATCATTATGCTGATGGAAAGAAACCATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTCCCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGIGICTGGAGTTTGTCTTTGTAACTCTCATCATCGAGGCTATATATAA
ESTC50	56	---	---	---	CTGTCCGTGGTAGCCCTGCCGCTGTCCATGGCCAGGGAGCCACTGGTGGGANCCTGGGCAGATG TTTACCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAGGACACCA AGT
ESTC57	20	---	---	---	AAGTGGGCCCTCCAGTCCNCTCTCTGGGCACAGATCCCACAGTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAAGTGTGAGAAAAAACTTCTCAAAATNGTCCAGACTTCAGGAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNITTAGCTACTTTTCAGAAATTGAAGGAGAAAATGCATTATG TGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTGGCTAGGCGTGGTTCTCATCTGTGAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCANAGGCCACGGCCAGGCTCGGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGT CACTTTCGGTAA
ESTC7	45	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCCTGAGTTGCANGCACGATGGAGATTTGGACACT G



[illegible]

EST10398 2a	147 C T ---				TGCTGGGTGGCAAGGCTGCAAAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTTATCTACTTGAITGATGATGTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTGTTTCTTCTTGGGCCAAGAAGGTAICTACCAATAGTGTCTATTAGGCATTG
ESTD-C7	14 G C ---				ATATCGTGGCCTTA[G/C]TTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---				CTTTCATGCACGATAGGCTTCTCTACTAATACAGAAATTTGAGAAGAGCAAAACAACATTTCAAGG ATAATGGGCAATCATTCTTTT[C/C]CTTCTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ---				AGTCTTCATCTGCGGTGTCAGGTAGATCCCTTTTACC[G/A]CCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ---				CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGGCGGCGCCAGGCTCACCTCTATAGTGGGTCG TATTCGTCCACAA[A/G]TGCACTCTGGATCAGCT
ESTD- HRASa	37 C T ---				CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGG[C/T]GGCGCCAGGCTCACCTCTATAGTGGGG TCGATTGCTCCACAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ---				GGAGGCAGGAGGTGGGAGGGGTCTGTCTCTCCAGTCCCACAGACCAGAGAAGCGGCCTCAGTG TATCCCAACCCCA[A/G]TGTGGCGCTGGGAGATGAAGAGGATTGATGCAGGT
ESTD-OTC	18 A G ---				GTGACCTTCTCACTTTAA[A/G]AAACTTTACCGGAGAAGAAATTAATATATATGCTATGGCTATCAGC AGATCTGAAATTTAGGATAAAACAGAAAGGAGGATGTAAACA
EST36751 7	36 C T ---				CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACTC[T/G]ATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACCTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109 A G ---				CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAGAATCTGCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTAAACAAT[A/G]TTTACCTTTGAAAAATAA ATGAAGGATTTGACCTGCTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTGAACAATAACA GATGCCTTCCCTTGTAGCAGTTTTCAGCCTCCTTACCCTA
EST18288 3	121 C T ---				GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA[C/T]GGGAGCCAGT GTGGACAGCACCCCTGGCTTCAACACCTACGTCCACTTCCAAAGGTAAGGCAAACTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ---				GGGAGTGACAGCTAGAGCACCAAGGGGGGCT[C/T]TACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATTTCTGG
ESTD-ALB	180 A G ---				AATCCAGCAGCTTTAGGAGGCTGAGGCAGGCATATACACAGAGGTCAGGAGTTTGAGACCAGTCTGA CCAACATGGTGAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGATGGTGGTGCATGCCTGT AATCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGGAGGCG[A/G]AGGTTGTGGTGAGCCGA GATGGCACCAATTGCACCTCAGCCTGGGCAACAAGAGTAAACTCTGCTTC

EST70523 3	182	G T ---	---	TTCCGGCCAGCCCCCATCCTTTGGCACCCCTGGTCCCTCAGGGGCCACCCGGCGCACTCACCGCTCT CGCTCGGTAAACATCCGGCCGGCGCGCTCTTGAGCACATAGCTGGACCGTTTCCGTATAGGAG ACCGTGATGGCCCTTCTGTCCCGGGCCTTGCCAGGGGCCAGCCCT[G/T]CAGAGAGGGGTCCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
ESTD- APOA2	101	C T ---	---	CCAGGTGTTGTGGCACGTGCCTGTAATCCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGAGGGGAGGTTGCAGTGAGCTGACATG[C/T]GCCACTGCACCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112	C T ---	---	CAGTGATCTGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGAC[C/T]CTAGAAGATACACGAGAC CGAATGTATCAAATGGACATTCAGCAGGAACCTTC AAGGATACCTGTCTGTGAGGCCAGGTTTATA GCACACTTGTACACTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST74167 6	137	C --- ---	---	AGACCATGAAGGAGTTGAAGGCTACAAATCGGAATCGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGACGGCGCGCAGCCCGGCTGGCGCGGACATGAGGA CGTGGCGGGCCCTGGTGCAGTACCGCGCGGAGGTGACGCCATGCTCGCCAGAGCACCGAGGAGC TGCGGGTGCGCTCGCTCCACCTGCGCAAGCTGCGTAAGGGCTCTC
EST43211 8	132	C --- ---	---	CGCTGGTGCAGTACCGGGCGAGGTGACGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCG CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGGAGAACGCC TGCGAGTGTAACAGGCCGGGGCCCGCAGGGCGCGAGCGGCCCTCAGCGCATCCCGGAGCGCTG GGCCCTGGTGGAAACAGGGCCCGCTGCGGGCCGCCACTGTGGGCTC
ESTD- ARSB	126	A --- ---	---	GGAGAAAATGGAGCCTGTGGGAAGGAGCGTCCGAGGGGTGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAAGGGGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAACCATCAGTGAA GGAGCCCATCCCCCAGAATTGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144	C --- ---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGCCAGTTGCCAGCTATAATCC ATCGAAATGATATTTTCATTGAGAACACCAATATTACAGTTGTGCTTTTCCATTATGAGTCCCAAAT TCAACCTCCCGATAGGCTGGGCTGACCACCAAAATATACTGGGTTTCTGTTTCTTTTCTTGATCAT TCTTACAAGTTATACTCTTATTGGAAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137	A --- ---	---	TAATGTAAGTCTATCCACCAAGCCCTGCACCATGTTTGGGTTGAGTGACATGTTCCGAAACCTGT CCATAAAGTAATTTGTGAAAGAGGAGCAAGAGAACATTCTCTGAGCACTTCACTACCAAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTTGCACAAAGACAAAAGCAAAGCC
ESTD- BA511	29	A G ---	---	GGGCAACATAGTGAAACCCCATCTCTACA[AG]AAAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCCAGCTACTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCCAAGATGGTCCACTGCA





ESTD- CB22	119 C T ---	---	GGCAAGTTTTATTGATAGAGAGGAAATCAAAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAAATGGGCAGTGCCAAACCCATAGGG[C/T]GGATACAAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCT AGTAACATAATTGCTTCATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C ---	---	TAGAACATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAACGTGTTCCCAACCCGA GGTCGTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAA
ESTD- CB24	145 A ---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCCAACCCGAGGTGGTGTGTTGAGCCATCAGAAAGCAGAGATCTCCACACACCAAAAG GCCACACTGGTATGCCTGCCACAGGCTTCTACCCCGACACGTTGAGCTGGTGGTGAATGG GAAGGAGTGCACAGTGGGTGAGCAGACAGACCCCGACCCCTCAAGGAG
ESTD- CB25	146 A G ---	---	GTTTCTTTCAGACTGTGGCTTACCTCCGTAAGTGAGTCTCTCTTTTCTCTATCTTTCGCCGTC TCTGCTCTCGAACCCAGGCGCATGGAGAAATCCAGGACACAGGGGCGTGAGGAGGCCAGACCCCTG TGACACAGGTAAG[C/T]CTACATGCTCTGTTCTTGTCAACAGAGTCTTACCAGCAAGGGTCTGTCTGCC ACCATCTCTATGAGATCTTGTAGGGAAGGCCACCTTGTATGCCGTG
ESTD- CB27	125 C T ---	---	TTTTGTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGTGCTTTCAGGAGTGTCTGTGGAGTCTGCTCATCACTGAC[C/T]TATCTTC TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAATGCT GCTTCTCTGTTTCATCCTGATGGAAGTCTCAAAACACCATTTCCATACC
ESTD- D4S338	59 A T ---	---	TTTTCTGTTTACCTTGTTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA[T/AT]GTA TTTCTTAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAAATAAATGTTA TTTTAGCTGTGAGAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGTGACCAGGTGTA TTGCCAATAAGCAGTAATATTTTGAGAGGAATCTTGTTTTCAATGCAGTAG
ESTD- CYP2D6	61 A G ---	---	CAGGCCAGCGTGGTCGAGGTGGTCACCATCCCGGCAGAGAACAGTGTCAGCCACCCTATGC[A/G]CA GGTCTCATCATTTGAAGCTGCTCTCAGGGTTCCCTTGGCCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D17S1873	40 A C ---	---	AAAAAACAATTTAACACCTTTTCAATCATATACACCAATA/GIATTTCCATTTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTAATTTGCAATCTAAATGTGATACTGATTAATGCAAGTTCAACAG ACAATTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---	---	CATCCCCAAGCCCATCTCTTAGCCACTGGCATTTTGGCCGCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGGCCCTACCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCGGTG GGGTGTGTGGCTATGTGGTGTCTGTGTAGTA[C/T]GGGGGCTTTGGTTTCAGTTGCACATATGGGTT ATTGCAGATTGCTTTGCTTTCCACCTTGAGCGAGCCCTC

ESTD- D17S33a	75 C T ---	---	CATCCCAAGCCCATCTTAGCCACTGGCATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGGCCCTACCCCTTTGATGTCATGGAAAGGCTCCTCTGGGGCG GTGGGGTGTGGCTATGTGGTCTTGAGACGGGGCTTTGGTTTCAGTTGCACATATTGCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCTGGCCAAATGGCGAAATCACATCTTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGCAGGAGAAATTGCTTGAACCCQA /G/GGAGGCAGAGCTTGCAGTGAGCCAAAGATCACACCACTGCACCTACAGCCTGGGTGACACAGTGGA GACTCTGTCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAATACATAATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAAATCCAATAAAGTACACTGTAATAAAGAAATTTAACAGAAATATCATTTGT TTATCAAACCTATTATCATTATTTATTGTTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTATTGCTGATGTTTGGCTGATGTTTCQJAGGAGCCCTTGATGTCATCTGTATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTTATTATTAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAAACCTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAGTGAACATACACTGCTCTAGAACCCAGAGTACATAGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAATATAATAATCTGTCTTTATTGGAAAGGATGCCTTGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAAACCTGACAGCCATTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAGTGAACATACACTGCTCTAGAACCCAGAGTACATAGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAATATAATAATCTGTCTTTATTGGAAAGGATGCCTTGGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTACAAAATGTATAATCCTGAACTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJAGTGCTCTCTACATCATCTTTCACAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGGACACCGAGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCCCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCTGGGGAGAGGAGGGAGTGGGAGGGAGACA GAAATGCTGATTJACJCTGTTGGAGAACCAAGTCTGCGCTGTGGGTAGGGGCAGCTGCTTCCAAG ACCTCTGATTGAGGAAGGGAGCAGCAGAGCGAGAGAGAACAGAT
ESTD-DMa	66 C G ---	---	GTGGGGACACCGAGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCCCTCCAC/ GTTTCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGAGTGGGAGGGAGA CAGAACTGCTGATTATCTGGTGGAGAACCAAGTCTGCGCTGTGGGTAGGGGCAGCTGCTTCCAAGA CCTCTGATTGAGGAAGGGAGCAGCAGAGCGAGAGAGAACAGAT

ESTD- DRD1	154 C T ---			TCCCCAGCCCTATCGGTGCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAG ACAAAACGGTCAGCACCCCAACCTGAACCTCGCAGATGAATCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGIC/TJCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C ---			TCTGCCTTTGGTGCAGGAGGCTGCCCCGGGAGCCAGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCCATCCACCCAGCCACACAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCCGACAGCCCCCGCAACCCAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---			AAGCATGGCCAGGATGAGCGGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCTGGCTGG CACCTGTGGAGTTCTGCCCCACAGGTGTAGTTCAGGTGGC/TJACTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGGAGGTGCGTGATGCCAAGGGGCTCTCTGTGAGGAGA
ESTD- ERBB2	93 C T ---			TCTTCAGGATCCGCATCTCGCCCTGGTTGGGCATCGCTCCGCTAGGTGTACGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCAAGTGC/TJGGGGCCGGTGCAGACCCACGCGGGCTGGAGGACTTCA CCCCGCTCACTCCGTTTCTGTCAGCAGTCTCCGCACTCGTGTACT
ESTD- ETS2	43 A G ---			ACTCACAGTGTCTTTAAGTGAATAATGGTCGAGAAAGAGGACCACTA/GJGGAAGCCGCTCTGGCGCCTG GCAGTCGGTGGGACGGGATGTTCTGGCTGTTTGAGATTCACAAAGGAGCGAGCATGTCTGGACACA CACAGACTATTTTAGATTTCTTTTGCCTTTTGCACCCAGGACAGCAAAATGCAAAAACCTCTTTGAG AGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTCAGAAGTAGTTTG
ESTD-F9	111 A G ---			AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTGTGTAAAGTATGATGTTTAA/GJGTCAAACTTCATTTTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A ---			CTTCCTATGGGATTGACTTTATTTCTCCTTGTCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAAAGGAAATAAATTCACAGTCAA AGAAATCAAGCACTTTTCGAAACATTTGAAGTTGTTTTGAACCTTGGTGCACCTTTAATTAACACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GDDH	200 C G ---			CGCAGACCGGTGAGTGGGGTGGGAGTGTGAGGGAAGGAGGGAACCTGGGGGTTTAGGACT TTCCGGGTGACTTTCCCGTTCTGTGCTTGCAGAGAAAGGGGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGACCTCTGTGTCGACCGTGTGTTCTGCTGCCCTGTTCAGCTGTCTGTCTGCCGCACTC/ GJGACTCTGTCCCGAAATTCGAGAGCT
ESTD-GCK	88 A G ---			GTTTTATGCATGGCAGCTCTAATGACAGGATGGTACCCCTGCTGAGGCCACTCTCTGGTCAACATGAC AACCACAGGCCCTCTCAGGA/GJACAGTAGCCCTGGCAGGAGATCCCCCACCACCCACACCTGGC TGGAGCAGGAAATGCCGAGCGGCGCTGAGCCCCAGGGAAGGAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCTAATTACTCAAAAGCTGTCCCCAGGTCACAG

EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAGAGGGGCCAGGGGTATAAAGGGGGCCCAAGAGACCGGCTC(A/T) AGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---	---	GACCCTAGTACCTCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCCAC(A/G)GGCATCA TTGAACCAAGTTTCCGTCAAGACTTGAATTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-HT2	154 G ---	---	GGCTAAATTTCCGAGCAACTTTCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTACAGAGAGATAAAGGATAAACCTGGGTTTTCTGTGC TTTGCTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAAAACAAGACACACCTT
ESTD-HT5	149 C ---	---	AACACAAAGCCCGCAGCAGAAITGAACTCGGACCCCTGGTTTACAAGACCAGTCTTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGTTTTCTCCCTTCACTTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATCCAGGATATTCCTCTACAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAGGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCAACCCCTCTTCTCTCCCTTGGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAG(A/G)CCCCAGA AATCAAGGTGGGCACGTCGCTACCGCCATCTCCCTTCTACAGGGAATTTTCAGGGTAAACT
ESTD- IGFBP1	43 C T ---	---	ACCCAGTGGAGCCCGCTCATTCACGCTCTTGGCAGGAGTG(C/T)CTGGGAGAAAGGAAGATG TTCCAGGACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTCAATGGATACAGAAITGTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCTACATTTGTGTGAGTGACGGGCGAGTGGTGATCCGAGAGTGTGGTGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACITTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCAATAAATGTTAGCTATTACTATCATATTATTATTATTTATTTTITG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGCAGTGG(A/G)CAATCTCGGCTCACTGCAAGCT CTGCCTCCTGGGTTCAATGCCATTCTCTGCTGCTCCAGCTCCCGAGTAGCTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTATGTTAGTACAGGAGTTCACCGT
ESTD-IL1B	99 A G ---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCAATAGCCCTCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTCTCTGCTC(A/G)GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGGTGGCTGGAACCCAGGCCAGCTCTGCAGCAGGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGGTGAGCCAGGGGCCCAAGGCAAGGACCTGGCTTCAGCTGCCTCAGCCCTGCCTGTCT(A/ T)CCAGATCACTGTCTCTGCAATGGCCCTGTGGATGGCCCTCTGCCCTGCTGGGGCTGTCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGGG

EST45311 0	151 C T ---			GCCCTCCTCTCTCCAAATTCGTGCCCTATAGTTTTCTCTATTAAAGTGAACATACATGCATCTTTTAGT GGATAGATGCACACACAAACACAAAGCCATTATGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGTCAAATC/TACCTCTTTCAATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80 A G ---			TGCCCCATCAGCGGGCGGAGACATGGCTGCCACAGCTCTTGAGGATGTCACCAATTAACCAAGAAAT CCAGTTATTTCC/GJCCCTCAAATGACAGCCATGGCCGGCGGGTCTCTGGGGCGCTGTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	26 A T ---			ATGCAGGATGAAGGTGGACAGGGAGG/GTJGAGGGCCAACTGTCTATCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 149 G T ---				ATACTAGTACAAGTGGTAAATTTTGTACATTACACTAAATTTATTAGCATTTGTTTAGCATTAACCTAA TTTTTTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAAG TTTTTTTTCTCTC/GTJAAAGTGCCAGTATCCAGAGTTTTGGTTTTTGAACGTAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGGTGCATGCA
ESTD- KRT10b	183 C T ---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAG/C/TJTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G ---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACATTACTTCTA/A GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T ---			ACCCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACC/C/TJTGCAACATTGACACA
ESTD- KRT8a	21 C T ---			ACCCTCACCCCTCCCTTAGCC/C/TJTGGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099 6	82 C T ---			CACCTGTGTGTCTAGATCTCCTCAGTGGCCGCTCTACTGGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TJGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTCTCCTTGGCCGCTTTGAGGTGG

ESTD-LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTCAAATTTGAACCGTAGCAAACTGCATTTGGTATTAGA AAATAAAAAATTTCCAATATGTAGTGTCTGTATTATACCTGCTGCCATGCAGCATCATAGCCTGT GGGAACC[G]GGAGGGCTTCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGACCCAGGCTTACCCCAATAGGTGAACATGGCTTCGAG AGAGTTG[A]CAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA
ESTD-LMP2	35 C G ---	---	A TACACACTTTCCCTTACCCATTCACTGAAACGACT[C]G[G]GCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACTCACCACCTCCAGCTTCTTCAGCTCTGCCCTGCTGCTGCCCTGCA AGGTTTGTCTTAATTCATCAATCAATGCTCTTCATCTTTTAG[C]TAGCTGTGGGTTTGTGTTG TTCTCTGTTTGTCTTAGTATCTGACTAGTCTTTTAATTAATAAAGAGATGTATCTAAACAAAAATAG AGATTGTATCAGAAGTTCACAACATTTATAAAAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTCTGATGCTGCTGCCCTCCCAAGCTCTGCTCCCTAG[C]TAGAACTTCAGGACAACGTGC AG
ESTD-METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAACACAGCATGCATCCCGAA TCTCAGGAAGTCTGTCTTCCAAAGGTTTGGTCAAGTTGCTGATTAC[C]TAGGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGTTCTCTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAC[T]AGTACCAGATCCACAGACTGATATGGCTGGT AACATGGACTGTATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCTTAGCCCCAAACGCTTATTGTGGT AGGATCAGCCCTCATTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATTCT GAGAAACTTCTTTTAAACCTCACCTTTGTGGGGTTTGTGAGAGAGTTATCA
ESTD-NFKB1	107 A G ---	---	TGTCCTAGGCCCCAGCCCTGCTTGTCCCTCCCTGCTTATCTTC[A]G[GTACTGCAAGAGAACACA GACAT
ESTD-NPPA	45 A G ---	---	GTGTTTCTTAATCTTTTCCAGGAACACAGTGACCATATTTCTTCTGCAGGCATATAGAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATACCTTTTGTGATTATATAGCAATTTGAGGG ACAAACCATAGTAGCAGAAATGGCTTGAATAGTAGTCTTATTTAACCTTGGCAATAGCATTG[C C/T]ATCCCTGTGGTTTATAAATAAT
ESTD-NRAS	202 C T ---	---	GCCACACACCCACCCACACCTCCACCTCAGCCAGACAAAGTTGTTGACACAGAGAGCCCC TCAGGGGCACAGAGAGAGCTGACACGCTGGGG[G]G[GT]CAGCCGTATATCATCGGAGGCGCCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTGGGCCCAAGTCTCTAGACAGACAAAAAC
ESTD-PA1	100 A G ---	---	TAGACAATCACGTGGCTGGCT

ESTD-PAR	120	A	---	---	CTCTTCAGGAACCAACAGTCTCTTACCAAAACACGACTTATTGCTGTCCGAGAGGTACAAACCCGTAGA ACTTCTTCTTAACGTAAATTTAGTTAAAGGAATCGAAACCTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTTCACCTTCTTCTAGTGTCTAGAACGTTTTCTAG GACTGGCAGTTTAAGCTTTCACITTAGGCTTCTGTATACCCATGCCC	
ESTD- Per/RDS	74	A	G	---	ACCTACAGACGTCGCTGGATGGTGTGTCCAAACCCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGA/GGAGCGTGGCGGAGACCTGGAAGGCCT	
EST68308	5	29	C	T	---	GGAAAGAGATTTAAGAAGCTTGATTGGAC/TAATCTGGTCTTTGAGTGTGGAAGAGTTTCATGTC TCTGCCCTGAGTTACAACAGAAATCCTTTAGTACAGCGAGTAATAGATAATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAGGTAAGAAAGTAGTTATTTTTA
EST54045	6	39	A	G	---	GGAAATTTAAAAATATTTAAAAATACCTCCATTTGCTTGA/GTCTTTTAGTGAAGATGATACCTGC AAAAGACATGGCTAAAGTTATGATTGTCTATGTGGCAATTTGTTCTTACAAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTTGCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
ESTD- PXMP1	88	A	G	---	---	ATGAAACATGGTCTTTAAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTTCTTTTTTTA ATGCAGAAAGAGGGGAAAAA/GJGAGCGAGCTGTGGTGACAAAGGTGTTTTTCTCAAGGCTCATAC AGATTCGAAAATCATGGTCCCTAGAACATTTGTAAAGAGGTAAAGTCTTATGAAATTTATAATCTT
ESTD-RDS	127	A	---	---	---	CCCAGGAATCTGAGAGCGAGAGCGGCTGGCTGTGGAGAAAGCGTGCCTGGAGACCTGGAAGG CCTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCAACCAAGGTGGAAGCCGAGGCGCAGACGAGG CCAGGCCACAGAGGCTGGCTGAGGCGCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCAC CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- s14544	94	G	T	---	---	TTGGGAAGTTAGAGCCTATATTAATTTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCCTCAGTTG/GTCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908	0	45	A	C	---	ATCACAGGCTCTGTGTCTGTGGCCATCATTTCTCTGGGAGAGATGG/JCJTGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST19590	55	C	T	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAAATGACATTGATGAGTGAAGATGT/JGGCTCAG GATGCCGGAAAAATGAC
EST76136	39	C	T	---	---	TGAAGCTTCTGCCACGCTTGCAATGTTTCTAGGAGAACCC/JTJGCGTCAACCTTTATCTATAGCCCTT CCCCTAGGCTCT
ESTD- SPTB	176	C	T	---	---	TGAACACCTGTGGTCCGGAGCCAGGTGTGTTTCTCTGGAGCCCTGAGGAGTTTGTGTCTGTGTG CAGTCCCCCGGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACTCTTGGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCTGTTGTGCACA/CJTCTCTGTGAAGACCCCAACCCCTGC CTCCCCACCCAAAGCCAGTTTCTTAGCAAGGGCAGGAC



ESTD-TAT	224 C ---	---	---	AAATGGTCAGGACCCTGATCCACAAGAGTGATGTAACCAATTCATCAGGGCCATCAGTTCAATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAAACTGAGTTCAATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACTTTCTCCAGATGGAATGGGATATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THRb	125 A C ---	---	---	TGGGCTTTCTCCGCGAGGTAGACTTCTTACTTGGCTGTGATTTCCAGAGAAAGAGTCCCAAG CACAGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAAATCACACAGGATC(A/C)CTTCAT CCACACTGGATTGGCCCAACAAGCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTCTGTCAGCTTCTGGATTCTTGTCCACCCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGCTCTCCAGATTTCAGTATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTTAAA CATGGGTGTGATCCATTTTCAATTTGGCCATAGGTCCCTATGGGATGACA
ESTD-TYR	122 GT ---	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCOCTACTCTTATGCAATAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTCACTTTATTACCTTCTTTCT AATACAAGCATATGTTAG(A/C)ATTAAAGTTCTAGGCATACCT
ESTD- TYRP1	222 A C ---	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCAATAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTCACTTTATTACCTTCTTTCT AATACAAGCATATGTTAG(A/C)ATTAAAGTTCTAGGCATACCT
ESTD- VB12	148 C T ---	---	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA(C/T)CAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC(A/G)TGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCACAGAGACAGGAACACCA GTGACTCTGAGATGTCAACCCAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

-188-

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAAGCCAGTCCTCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGGAGAACAAAGACAGCCACAGTGGCGGGGATGGCGGGGAGTTCC TGTTGCGGCCACGGCTGGCTCGTTGTGAACGGTAGCCTTTCGGTTGCGATGCCTAAACCTTTGT TTCTTGGCCAAAGGAGGGGGTGGCCATGCCTGAGATGTAGATGGGCC
ESTD-VWF	36 G ---	---	AGGTAGGAAAAGCAAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTCCACACTGTCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTCAGCTCAAGCCTCAGCACCCAGATGCTGTTCTATAAGGATGACGTGCTTTTACAA CATCTCTCCATGAAGAGCACAGAGAGTTATTTATCTCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAAACCACTGCAGAGTACCAGTC/GTGTGGTGGGA AGGAGTGGCCAGTCCAGGGTGACACTGGACAAAGAGGGCCATCCAAAGG
ESTD- TNFAb	152 A G ---	---	TTCTGCATCTCTGTGGAAGTTAGAAGGAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGAAGGGCATGAGGACGGGTTTCAAGCTCCAGGTCCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTC/GAATCGGAGCAGGAGGATGGGAGTGTGAGGGTATCCTTGATGATG CTTGTTGTCCCAACTTCCAAATCCCGCCCGCGGATGG
ESTD- TNFAa	88 A ---	---	TTCTGCATCTCTGTGGAAGTTAGAAGGAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGAAGGGCATGAGGACGGGTTTCAAGCTCCAGGTCCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGTATCCTTGATGCTT GTGTGTCCTCAACTTCCAAATCCCGCCCGCGGATGG
EST52418 6	113 A G ---	---	CAAAATACAGGGTCAACTGCTATGATGTTTGGAGCCCACTCACCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACT/GAAGTGAAAACCTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACCTATTTGCCAGCCCCCAGGGACAGAGCTGATCCTTGAACCTCTTAAGTTCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC/GGAGGCTGGCTTATCAGCCTCCAGCCAGACCTGGCTGCAGA CATAAATAGGCCCTGCAGAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCTGCTGCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAAACTGGCCCCCATCGGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAAGTCAACTCCTCTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAAG/ATCTCTCTC CCTCCCTGAGCTGGAGCAACAGCAAGAACAGCAGCAGGAGCAGCAGGAGGAGGTGCAGATGCTG GCCCCCTTGGAGAGCTGAGCTGCCCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCATCTTGTTCGAGTTT CTCTGCCATGTTGCTATTGAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCC/GTAAAAACATCTATGAGCCAGGAGAGAGATTACGTATTCTCGAAGCGGGGCTATGTG TCCCGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	AGACCTCAGTTTCCTCTGTATAAAGGGAAGTTTGTTCTTGATCTCCATGGGCCAGC/C/TJAGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGGACAGGTGGAGAGGAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGGAATGTGG
EST39852 8	106 C G ---	---	CGGCTTCCTCCAGGTATTGTCAGAAAGCCGAGATGACCTCTATGTCTCAGATGCATTCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTT/C/GJGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAGGCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	ACCTGGGTGTTGCTGGTGCTGTGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCTGGGGCCCGTGG TCTCTCTGGTGTGGTAGTCTCTGGAGTCAACGGTGTCTCTT/GJGTGAAGCTGGTGTGATGGCA ACCTGGGAACGATGGTCCCGAGGTGCGGATGGTCAACCCGGACACAAAGGAGAGCGGTTACCC TGCCAATAT
EST36027 2	120 A C ---	---	AGTGACTCCAAAGGAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCAGCTACCACTGCAAGAACAGCATTCATACATGATGAGGAGACTGG/CJAAACCTGAAAA AGGCTGTCAATCTACAGGGCTTAATGATGTTGAACCTTGTCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGATAGTGGCTGCTCTAAAAGACAAATGAATGGGGAAGACAA
ESTD- COL2A1cc	112 A G ---	---	AGAATGTATATAGTCTCAACTGGCCATCTCCATTTTCAAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCTCTGTCACCTT/CJ/GJGGGTTCAGGTGGAAAA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTTCAGGTAAGTCAACTCAAGCATATACAATACTGCCT TTGTCAGCCTATTGAGCTGTAATCACCATAACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTGCTGGGACCTGGAACA/CJ/TJGGACTTCTTCTACTGCAAGCAGACAAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCACAACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	GCCGAATGCCCGGAGTTCTCCAATGTGTGGAGAAGCCCTTAGAAGACATGTTTGATGCTTAGAA GGCAATCCATCAAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCTCCTCATCATGAAAAAC TGGAGGCCGGGCAT/GJGTGCTCATGCCTGTATCCAGCATTTTGAGAGGCTGAGGCGGGTGGAT CACTTGAGGTCAGGAGTTGAGACCAACCTGGCCAACAT
EST12274 0	135 A G ---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAAATAGAGCCCTTACCAAAGTGAT TACATAAAGAAGTCAAGTGGTTTACTCTCTCATGACCAAAATATCTTCCCTCCTTAGGATGAGGTG A/GJTAGTAAATGACCGATGGGGTCAGAACTGTTCTGTCCACCATGGAGGATATACTAATGTGAAGA TAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G ---	---	ATGCTAAGGGGATCGGACATGAAAGGACCTGTGAGCCGATTGCTCTATCTCCAGGGCCCTGTCATC CAGCTCACTCATCAATGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTGTCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	---	TTACATTTGTGGATTGTTCTTTTGTGTCAGCACCTTTTCAACATGATGTATGCCCATTTGTCCAAG TTTGCTTTGGCTGCCGTGCTTGTGGGATATTTGAAAGAGATC/TJTTGCCAGTCCAAATGTCTCTAGA GAGTTTTCCCAATGTTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATT TTGATTGATTTCTGTA
ESTD-RYR1	109 A G ---	---	---	CTTCGTACGGGAGGTCACGTCCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCAATTTCCC CTGCTGACAGTGATGACACGCGAGACTTGTCTACTATAG/A/GJGGGAGCTGTGTGCACTCATGCC CGCTCCCTCTGAGGCTGGAGCACTGAGAAATCAGCTGGAGTGGAGGCCACCTGGCTGGGCGCCAGCC ACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCCCTTACTCTCTGCTGCGCTGCAGGATGTG CG/A/GJGCTGTCCTGGAGTAGCCCGGACTCTTGTACGGTGGCATCTGAGACCAGTGAGAAACGCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST44438 7	100 C ---	---	---	GATAAGTACACTGAGCCCCAGGAGGTTATTGCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGGCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGGCGGTGCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGGACAGGAGATGGGC TGGATGAG
ESTD-PBDA	103 A G ---	---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA/C/TJG TCCTGCTCGACCTAAGCGGAGAGCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	122 A G ---	---	---	CCTTCATGCCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAAJAVJTCCTACCCGCGACTTGTCTCGCATACAG ACGGACAGTGTGGTGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48 A G ---	---	---	TGCAAAACACACAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAG/A/GJTCAGTCCA AGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTTGAATGTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-ACE	96 C T ---	---	---	ATGGCTTGCCTTGGATTTCAGCGGCAAGGCTCAGCTGAACCTGGCTJAGJCCAGGACCTGGCCCTG CACTCTCTGTTTTTCTCTCTTCATCCCTGCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGT GGTACTGGCCAGCAGCGGAGGATCGCCAGCTTTGTGTGTGATGTCATCTCCAGGCAAGCCAC GATCAAGCAGTGCACACGGGTACGATGGACAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC/C/TJGTCTCCCTGGCTGGGGGCCAACCCCGGCTTCCA TGAGGCCATTGGGACGTGCTGGCGCTCTCGGTCTCCACTCTGAAACATCTGCAAAATCGGCCCTGC
EST54419 8	88 A G ---	---	---	CTTCTGCCTAATTTGAATGATATTGTGCTGTGGGACCTGAGCACCTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACJAGJATCCTGGGAGATGATTTGGGTTAGCGTGGTCTGATGTTGCTA CTATAGTCCAAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGGAGTAAACTTGGATTGGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACAAACCATAGCCTAGJTTCGTAGCCATATAATTTGGTTTGTGCTTAC ATTATTACTCCTTGCCATTTCAAGAAAGCATTGCCAGCTCTCCAACTCCATCACCCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	GGCTGCCAGGGTTCCGTGGAGGGGSOCTAGCCGGGCCCTGCTGGCGTGGCGGTGCTGGCCACC GTGGAGGCAACCTGCTGGTCATCGTGGCCATGCCCTGJGGACTCCGAGACTCCAGACCATTGACCAA CGTGTGCTGACTTCGCTGGCCGCGAGCCGACCTGGTGATGGGACTCCTGGTGTGCCGCCGCGGGGCCA CCTTGGCCG
WI-567b	48 A G ---	---	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCCTTGGTTCAGJAGCCCTCATCTCTTTA CAGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGTCTCTTCTCCAATCCATTTCTCAAAAG GCTGCCACTGTGATCTCCCAAAGGTGATCTGATGCTACCATCTTGCITCAAGCC
WI-801c	58 G T ---	---	ATGGAACATTTCTTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/JAGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCCACCAGAGAGTTAA CATTTCTGCCACCCCTC
WI-801b	58 G T ---	---	ATGGAACATTTCTTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/JAGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCCACCAGAGAGTTAA CATTTCTGCCACCCCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATTTACATTAGTCTCATTATCTGAAATATTAT TTTTTACA/JGTTACCCCTTTGATTTTGTGATTCATTTGTAACGAGAGATTACAATATCAGTAACGC TGTTTCATTGATAGTGCTATCACAATGTCTAAATACITTTTGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTATGGTTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATACCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA/C/TCTTAACTGCTGCCCTTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGAGGTAAAGAGGAGACAACCTGTGCTTT TTAAGAAATAGAAGAGTCACTTTTCATTAGAAATGGCTTTGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGGCTGTCTTCCCGAGAGGCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCCTATGAGGTAACTGAGGATGAAGGA GTGAGTCAATATTGGGTGGCAATTAATGACCCAGCCTCCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG/C/GJAGCAGAAGCAGCAAGGAGAAAGGAAGT

WI-2625	98 G A ---	---	---	GGCAGTCTGGCTGTAGTGACAGCACTGAAGGATGGAGGAGAGAGAAACAGGCAGAA GCACTGTGGTAGTTACAAGGCTTATTTAGGA[G/A]CAAAATGATGATCTCCCTGAGGACTCGCAG AAATTACCAGCAGTGGACAGGGTTATCTGTGGTGAATTCAGTTATCCACTTCGAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54 G A TAGG	TGACCTTCCTA GTCCTCTCTTA	GCCCTAAGTGT AATCACAGGG	TCCTGTTGTCATATTTCCCTCTTTGACTCTGACCTTCCTAGTCTTCTCTTATAGG[G/A]ACCCTGTGATT ACACTTAGGGCCTACCTGGATTATTTAGAACAATC
WI-2939	72 G T GTGCCTTT	GGCTTGCTCA	CTTGTTGAGGG AAGGTCTTG	CCATTGTTGAGTTGGTGGGGTCACTTGTCTATCCCTCGCACTCAACAAAGTGGCTTGCTCAGTGC CTTT[G/T]CAAGAACCTCCCTCAACAAGAATGCTTCCATGCTCCCGTGTCTTTGAAAAATTCGACT TTATCCTGAAAAACTCAGCTGCAGTGTATCTCCGGTATAAAGCCACTCCTG
WI-3203	99 G A AGACGAG	GGTTATGCCGC	TCAAGTATTGC CTTGTTGGG	CTTGCTACCATGCATTTACAGCATACAACCTCAGTGAATGCCGTAAACCCCATTAATAAACAT CTTGCCATCGAAGGGTTATGCCGACAGCAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGA GAATAAAGATTTTGGATGGATGAAAGCAGAGAAGGAGATGCTAAAAGTGA
WI-3473	101 A G GGCCTAGGGA	AAGCATTTTA GGCCTAGGGA	CCTGATGTCAC CAACATTTCT	GGAAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTGATAGGCCCTGTTTGA GATTGCAGAGAGGAAGCAATTTAGCCCTAGGGA[G/T]AGAAAAATGTTGGTGACATCAGGGCT ACACACTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTTGGCTCCCC
WI-1796b	29 A G ---	---	---	ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATGTCTTGGCTCCCC
WI-1796	29 A G ---	---	---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCCTGCAGAGTAGGAAAGATGGGGTGAGT AGTCACATTAGGTATTTTCCAAATAA[C/T]AAAATGCCCTCTGAAAAATATCTCTCCCATGTCCCCTGTC TAAATATAACATTTTCCC
WI-4360	93 C T AAATAA	GTAGTCACATT AGGTATTTCC	GAGAGATATTT TTCAGAGGCAT TTT	GCTGAGCTTTTGTGGCAGAGCCAGGACAATTCAGCTGCCGGATTTTAAATAGATTCTGCAGCACTGCAA CAGGAACCAAAAATCAGTC[C/T]GGGTAACCTGAGAGTGGTTTTCACACCCAAA
WI-1959b	87 C T ---	---	---	GTTGTGCTGTAGCAGACACAGAGGCA[G/A]GAGAGGAAAAAGCCTTTTTGGTCCAGGGGCTTACAG TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGGTATAGGGTTTG
WI-1973b	28 A G ---	---	---	CTTGAGTATGCGTGGATTTTGGTATACACAGAAATGGGAGAGCTGGAACCTAATCCCCCATATACCA AGGGACAAATGTATCTGTTCTACAATTTACAGTAGGAGACATATGTTCCATGACAATGGTAAT TTTTAA[C/T]GACAGTTTTTAAATTGAGTGAAATACCATAAAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCCTATAAATAGC
WI-1980b	140 C T ---	---	---	

WI-2015b	190 A G ---	---	TGTCAGATAGTCGCTCTACCTAGGTGCGAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACACAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGTCTTTTCCAACT[AG]CATATACTT CTAATACCATAGAG
WI-754b	49 C T ---	---	GAAGGCACAGGGAGAAGATGGCTGTCATCTACCAGCCAGGGAGAGAAAGC[C]TACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAATTTGTATTACITTAGA
WI-754	22 T C ---	---	GAAGGCACAGGGAGAAGATGGCT[C]GTCTATCTACCAGCCAGGGAGAGAAAGCCACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAATTTGTATTACITTAGA
WIR-1b	56 A G ---	---	AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAACTCTGATGATCGTACATCC[AG]TGGCGCTG GAGGGTGATGCCTCCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-1	56 A G ---	---	AGGCAATCAGACCTACAGAAAGGAAACCCCAATAAAACTCTGATGATCGTACATCC[AG]TGGCGCTG GAGGGTGATGCCTCCTGAGGACATGGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-3b	72 A G ---	---	TAATTTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT[AG]TCTAAAGTTATTAGCTCAGAGCCTCACACATCTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---	---	TAATTTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA[AT]GTATCTAAAGTTATTAGCTCAGAGCCTCACACATCTCAGTACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T ---	---	GAGCCTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATCCCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209 C ---	---	CGGCACAGAGACACAGAGAGAGTCTGCGAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5f	196 C ---	---	CGGCACAGAGACACAGAGAGAGTCTGCGAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5e	194 C ---	---	CGGCACAGAGACACAGAGAGAGTCTGCGAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5c	177 C	---	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5b	159 A	---	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGTGT AGGTTTGAAGGGAAGGCAAGGTTAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAC AGGTTTACGTCCAG
WIR-5a	37 A	G	---	---	TAACCCCTGAAACCTTTGCTCTCCTCATCTCAGGGAGAACACAGACTTTCATGTTAAGACCCAGAA[VC] CGCAGTCTGGGGTGGGCAG
WIR-6	63 A	C	---	---	TTCTGACTATT[C]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12 C	T	---	---	GGCGTCTCTATGACTATCCTGGTCAATTGACTAATGATTCCTG[C]GCCCCTTG
WIR-8	46 C	T	---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAGTTGTCAGAGAGGATGA[C]G]CTGAAG AAAGAACTACTCTCTTTGACCAATAAATACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WIR-2	56 C	G	---	---	TGTCCTTGCTTATGCCTGCTCTTCGCTTGGCAGGATGCTGTCATTAGTATTTACAAGAGTA GCTTCAGAGGGTAACCTTAACAGAGT[G]A]TCAGATCTATCTTGTCATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCCTGTTCTCACTC
WI-7069	93 G	A	---	---	GGTCATTTCCTTTTATCTGTCAGGCAGCCAGCTGACTTTA]TCTCTCTGTTCTGTCATCTCCCC CCACATACCAACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A	T	---	---	CACACTGTTACACACCTATATTTCAAGTTTGGAAATGC]A]G]TATTTGCAAGCAGCAATACAAAAGTA TTCATGAAGAATGCATAATCTCTGAAAAATTATGAAAAACATCCCT
WI-18612	37 A	G	TGC	---	TTGATTGCTG CTTGCAAAT



WI-18517	87	C	T	CAGCCTGA	CAGGAATCAG	TGTTTGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCCCTCCATTGTGTAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA/C/TJTGTCACCTTGTCACCAACACAACTGACTGC
WI-18668	76	C	T	TAGGCAAAA GC	GGCGAAAAAC CTGCACTTTT	GCTAAATTAAA CTGCACTTTT	CGATTGACAACCTTTTATTTTCAACTAGGTACAGTCCAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAA/C/TJAGCAAAAAGTGCAGTTTAAATTAGCAAAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T	C	A	AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGAAGCATGCATCCCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT/CJGCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A	C	GGGTAC	GGGTCTCCGA	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTGTGCGAGCACCACACCAAGGGGAGGTGGGCTTGAAGGAGCC CTTGAGGAACACGGGTTCTCCGAGGGGTAC/CJCCAGCAGGGGCTTCAGCTTAAAGTCG
WI-18673	29	A	G	---	---	---	TGTGGCAACCTTGTTTTAATTGCAAA/CJG/ACTTAAATTTACAGCACATTCATAATGAACCAAC AGGAGAGTTGCTGACTTTGTACATATGAATATATAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T	C	GGG	GTGTTGGGTG	GCAATACCAC TGAAGAGGAC	ACCATGTCATGTTTTATTGGAGGTTAATTCCTATTAGGATATGAAAGGATTCAGCAACGATTGAGATT GTGTTCTCAGGAGGGCTCGGGCCAAAGTCTGTGGGTGGGGGTGCAGAT/CJGTGTCCTCTTC AGTGGTATTGGGACC
WI-18533b	91	T	C	---	---	---	GGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTTTAAACTCCCCGAGATTTCCTTTTATT TATATTTTCATTTTCATCCTAA/T/CJTACTGAAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T	G	---	---	---	GGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTTTAAACTCCCCGAGATTTC/TJGJCTTTA TTTTATTTTCATTTTCATCCTAA/TTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A	C	TTC	TCATCTGATAC CTTGTTCAGAT	AACGAGATA AGGTACAAC	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTTCATCTGATA CCTGTTCAGATTTC/CJAAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAACTTT
D49493	159	A	T	TCGGGAAT	CCTGAAGGAA	ACTTTCAGGCC AGGGC	CAGGACTTGTGGTGCAGCTGCAGACACAGACAGCAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGGTCTTTCATTGTAGTACTAGGCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATTA/TJGCCCTGGCCTGAAAGTGGCCCATCATTCATACCCACTGT CT
EST10030	98	T	C	TCAGTCCC	CATTTTGTTC	GCAGTGGTGGT ATGGATGA	TATTTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCT/TJCTATCCATACCACCAGTCTGATTG
EST10052	24	G	A	GAGGCTG	GCTCACTTCTG	TGTGGAACCTC AATCTTAGACT	TATTTGGCTCACTTCTGGAGGCTG/GJA/GAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCAATAACCTGGTGAAGTCAATCATGTGGCAAGAGAGAGGGCTACAGAGCAAGAGGAA A

EST10605 2	118 C G ---				CTTGCGTAAATCACAGTTCTGTATTATACAAAAACITTTGTTTTCTCTGACAAAAGTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT			CATGTGCAATCCCATGATTGAAAAGACATGTGCTCTCAAGTAGATAAGAGGCATAATCTT[G/J]AA ACAAAATCTTTCTGAAAATTTAGCTTATGAACCTCATTAACACTGCAACCCAGAGAGGAGGCAC TATGGAGCCAGAGGAAGTGACACTATATGTGGAAGTCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11260 8	101 G T ---				TTTGATGGAGAAATCCGAGGCCCTGCCAGCATCCCACAGTAGATTCTTTGGACGAAGAAAAATCCT TCTGTGGATTGAGCTTTACCGCCTTCTCTCATCTGCTGGT[C/T]TCTCAGAGCTTTAATGTCCGT CCTGCTCTCOGAGTCAG
EST11349 9	109 C T ---				GAATCTGGGTATTAATAGCGGTGCCACAGGAGCACATAGGAAGAGCATCCAACTACTTTGGAG CCCT[G/J]AGGAGTTTTAGAGAAAGCTGGAGCCGGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGAGGAAGGAGTGGAA
WI- 16632a	71 A G ---	CCAACTACTTT TGGAGCCT			CCAGGAATAAAGAAAAAGAGTCAGAGGAACAGCTTTTGATGTTATGAGGCTGAGACACTACTC TTCCCTCA[G/J]GACTATTTCTGACTATAGTGATAAATACATTGAAGACTTCAGGAGCTCA CTTGCCATTTATTTTGTGCATGTTCTTAAAGGCTTGAAAGATAAATTTGGAATGTGGGAAC ACATAGATCCCAGA[G/A]TTTAAAGGGCTGGAAAAAGTAGCCTTAAGAC
EST11772 6	74 A G ---				AGAGCAATGGTGGATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAAGCTCCACAGAACTTTCATGCACCCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST11795 3	82 G A ---	CAATAAGCAG CTCATTTTGAT TAC			GOCTAGTAATCCAAAAGGAACATGTTTGATAATAACACTCAGTACAAAAGTCTGT[G/J]ATCCAGG AAGTGACCAGCCCGACGCTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC GTGAAAAATTTTTATCTGTACGCTTTCC[T/C]ATTATATTTATCTTGCTCTTGATTTCAGCACCC CACCGATTTCAGGCAGTCTTTCTAACTGTGCCCTGTGAGCTGTTAAAAAGTCTCT
WI-16644	42 G A TAC				CCCTAGCAATGACTTGGAGTTGTGTCCTCAATACCAAGTTACATACTGTGGCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACAGATTAT[G/J]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTTA
EST12005 9	56 A G CAAAGTCTGT				ATCTTGAGGTTTCTGGGCTGTGAG[G/J]AAGTGACATCTTTTACTTACCACAGGTGAGGAACCCAT AAAGAACTGTGTAGAAAAGATATCAGGTGAGACTTTTTAAAGGGCTTCTTATCAGCTCAATAAA
EST12055 9	32 T C ---				
EST12492 1b	95 A G ---				
EST12492 4	25 A G ---				

EST12502 2	52 C G ---			ATACTAGGGAGAAAAACCAACTGGAGGGAAGTCCACAGGTCCACACTTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAGAAATGCTACGGGGGAATGAOCCATTTTAAAGGCCATGTG GTCGTCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAATGTATCGGTAAAAAGAAATAGGAATGCATATTTCAACTCACTGTCAAAA CAGGTGTTTATTATCCCAATGACAGTGTTCCTGAGATTC/GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTCATTTATTCATTTGTTCAAAACACACTGTCTAGTACCAACATTTGCCACCGGC[A /G]TTGAGAATACAATATTGAAGAAGAGICACTGCCCTCTGGAANAATCAGAGTATTTGA
EST12817 9a	22 C A ---			TGGGGTTCTCCAGGATCCAGIC/AJCTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTCTTGGGAGTGACCGGGATGGGAATCCATGTGCTTTGCGTACTCCATCAGGTCAATGCG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCAGTATTTACCAGAAATTTGTTTGGGTTTCA ATGTAGTGTTAGCTTTAATACACTGCACCTGTTTIG
EST12949 2a	52 A G A T A C T G T T	GGCTTTAATCA TAACCTAATA	TGTTGCCCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCAACCTAATAATACTGTTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATTCCTCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTCTTAATGAAGCATAATAACAGTTAAAACTCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACA[C/T]GGAGCAGAAAGCAGCTTCCCACCCCAAG CACTCTGAACT
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTTTTAAAAATTTAATCGCTTTATACAATTGACACCAATAAATGCAC[A /G]TATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCCTTCATAGCTGCTTAGGTTTGTCTTCC[C/T]AGCATAATTCAGCTATAATCA CCTACATTCCTCCACAATATTTCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATT[T/G]GACTAACAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A A G A G A C G C	GCTCAGATGTG	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTACAACCAACTGCCGCTCAATATGCAGCTCAGATGTGAGAG ACG[C/G]ATCTCTGTACAGGCGGCTACTGTCTTCAATCCTTTGCAATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C T C T C A G G C C T	AACCAGATTT TCTCAGGCCT	ACAAGAGGGTT TGACAAAAGA G	AAAGATATAAAACAACCTCCCATCAGTAGGAATACAAGGTTATACATTTTAAACCAGATTTTCTCAGG CCTT[C/T]TTTGGATACCTTTAGTAACTCTCTTTTGTCAACCCCTCTTGATATAACCA

EST13278 2a	51 A G	CITTCACCGAA CAATAATTTAG G	CATATCTTGG GTGGTGAGAA	TTGCGAGAACGTTTACAAGCTCCAAACCTTTACCCGAACAATATTTTAGG[A/G]ATTTGAAATTAT TTCTGTAGTTCTCACCAACCAAGAAATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTCC AGTCCAAAGA	GATGGAAAATT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAAAATATTTAGATAATACCTGTGGGAAAGTGCTGAATTACTAGCC TGCCTGAGAATCCACACATTTTCAGTCCAAAG[A/T]AACCTTCCTCAAATTTTCCATCTCCCATCAGA GG
EST13290 9		CAATTTTITAGA AGTTGGGTTT	AAATCACITTC TGGAATTTCA	AGCTCATCTGCAAGCAATTTTITAGAGTTTGGGTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTTCACTTACTTAAAGACCTAAAGACAAAGTGATCACATCACATATATTTTGT ATGTGGGGCTTTTITG
EST13518 2	39 A G CTT		G	GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTCAGCATT[A/C]GACTTTAAAAATTACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCCTTATAACCTTGATTG
EST13522 8a	45 C G		---	CAGGTTGGTATTCTCAACTAGGAGCTATTTTGGCCCCCATCCCCCGGCGAGTGCTGGAGAC[A/ G]GTTTATTGTCACAACCTGCGAGAGGTGGGTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	66 A G		---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGGCCAATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGAGAGGAGGTTGGTGTAGTTGAGGGAGAGAAAGTTGGAAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	69 T C		---	AAGATTACGGACCATAAGAACTGCCCCCGACCCATACACACACAATTTATAGCAGGTAACCAACCAA CTGAAAGGAACAAAGTAATGACTTCTTGAACAA[A/C]GTTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	101 C G		---	CCTCAACCATCTGTAACCCGAGCC[A/G]CAGTGACCGGACTTGCTGCTTCCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	25 A G		---	CAATGGTGTCATGTGAACATAT[A/G]ACCTATTATCAAAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCGAACAGGAGGGTAGGAGG
EST14221 5	23 A G		---	AAATCAATGCATTTGTTGGCATGCTAGACAGAGGCATT[A/T]CTTTTGAAGATCTTTTAAAAAT ATTTTGACTGTTCCCCCTCACACTCATTTTAAATTGT
EST14812 2	42 T C	GCATGCTAGA CAGAGGCATT	AAAATATTTT AAAAGA	TTCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCCGGAGTTTGCCTTTTCTAACATTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	50 A G ATA		TATGTACT	TTTGCTCGGCAATACATAGTGGCAATGACGCGTGAGTTCGGCCGCTCTCCCACTGAACCCAGTAAT TCACCAGACAATGGCGCAACCACTTAAATAAATGCTTCCCGTCTACACCCACCACTACTGGTT[A/T]TTCC GGTACTGTTTTCCGTA
	128 A T	CATACCCACC ATACTGGTT	CGGGAACA GTACCGGA	

EST15420 6	109 C A ---			---	TTTAAACCCCAAGACCTTGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTCATCATATAATCATATAGCCAAGGGACT[C/A]GGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCTCAGG
EST15700 6	48 G C GGA			GGATAGCTGA AACAGAGATA TTATTCTC	GTCACCAGCACATTTTATTAAAGACGTGAAGAGACAAAGACAAACAGAGGA[G/C]AGCAGAGAAATAA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC			GATAGTTGATG TTCATTATTCC CTATAA	AAGGATTGAAACATACCTAGATCATATAAAATTTGTGAAGGTTTTGCCATCACAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAAATGGCTCCCAAGGT
WI-16782	96 C T CACTGTAAGG TC			CTTCTATCTTT CTGTTCTCTCA TC	CTTCTCTCTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGGA[C/T]GATGGAGGAACAGAAAGATAGAAGAGTTTGGGGT GCTGATGAAATTTGGGGG
WI-16783	64 A G G			CTGCTTGGTTC AATCCTTATTA G	AAAAATGTAAACCTTAGAGGTTGCCTCTTTTGTGTCACTTTTCTCTGAGATGTCTTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACCTCGAGT
EST15948 2	58 T C ---			---	CAGGACTTAAGTCAATTTTGCCTGGAAGACTTTAACTAAAGGTGAGGGCAACATAGGAAT[C/T]GTGA CAGGACCACTCGGACCAGGAAGTGTGAAATCGTCACACTAGCGTGGCCAGCCCTTTTTCCTGGG TGCTCTGCCTCCAGAGC
EST16088 8	89 G C ---			---	GGTTTGAAGACGCGCTTTATCTCCACCTGCCACTGGGATCTCATTTTGAAGAGCTGTTTGTGAGCC TTTTCAGAAAGGCCGCTC[G/C]GGGTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T ---			---	CGTCTGAAGTTTCTTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC[C/T]AAAGAGGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ---			---	ATCCAGCTGTGAAGGACAGGAG[C/G]GTAAACACAGTCCATTATAAGGGGTGTGCACATTCCCA GGGGCTCCAATAATGCAACATTGTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---			---	TTCTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGGTTCTCTCCAGGA[A/G]TTGGCCCCGAAGCTGGCTCAGTTACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---			---	ATGGTATAACAAAATCAGTTCCAGGTTTCTTCTGAACAAATGATCCTTTGGTCTTTCCCGTGGCATG CTCCTAAAAACAACCTAAACAACCCCTCTACGCTAATCAGTCACCTAAGATA[T/C]CGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---			---	ATGGTATAACAAAATCAGTTCCAGGTTTCTTCTGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCCTAAACAACCTAAACAACCCCTCTACGCTAATCAGTCACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ---			AGCCAAATTCAAACGAACTCTATCAAAACACACAAAGGCCTAGAGGAGATTAT[C]TAAATGAACGT AAATAATTCAGGCAATTTTGATCTAAAGCATTTTGCTTAGCTCTACAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGGTAGGGAAGATAGTAGTGTCAAAATAAAATGGTAAACACAGCAG[G/A]AAATGGAA TTATAGCTTCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGGCAGAAAGTAGTA
EST16183 2b				GCAGGTAAACTGTGGTTCACAAAGTATTGTTCTTTCAATAAGAAAGAAATATCTAGTT[G/A]GTAG AGGAAGGCACGTGCTTCCTGGCCCTTCCTGTTTCATATTTTATGTCACTGTCTTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	59 A G ---			AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTGCGCATTT CCCCAGAGGAAAGTCAGCATCATAAACACATGGGTACATGCTCAGCAGCATGGTGTGTC
EST16229 2c	28 G A ---			TGTGAACCTCGAATTCGCTTGTCCTCAAGTCTGAGTCACAGTTTCATTTGGGAGT[C]CCCTGTGCAGOC CTTGCCAGTTCCACGAGGAGGATACCTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
EST16229 2b	52 T C ---			TGTGAACCTCGAATTCGCTTGTCCTCAAGTCTGAGTCACAGTTTCATTTGGGAGTCCCTGTGCAGOC CTTGCCAGTTCCACGAGGAGGATACCTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
	45 T C ---			CAGACTTTTCTCACACCTCATTGGCTGGAAGTGGTGCATGCACATCCTTGAACATCATTTGGCAA AGGGAATGGTGCATCAAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA[G/A]CTGTCC TGAACAAAATCTAGGCTC
WI-16816	124 A G TGGGTTA	GGAGCCATTGT	GCCTAGATTTT GTTCAGGACAG	GCCACTCTCCTGTGGCTTGCTCCTGTCCAGCTGCTGCCAGTGCCACA[G/A]TGGTCTAGCCTCATGG CAGAAGCATTTAGCCAACTCCTGGTGTGCTCCACTCTCTTCTTCCGCCGCTGGGGCTCACCACC TCTTCTCCTCAATC
EST16269 5b	49 G A ---			GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTTGTTCTTATGAAGAAAGTCAG AAGCTGATAAAGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGGA GCCTCCATTATGGGAATA
WI-16824b	83 G A ---			GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTTGTTCTTATGAAGAAAGTC AGAAGCTGATAAAGTGGGCTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGGA CTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTG	CAGCTTCTGAC TTCTTCATAAG AA	TTGCTTTTATTAAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTATTACAAA AATGGCTTCCAAACCATTAATAATGAACTT[C]GGAATAAGAGCATAAACGGAACAGTAACATCA
EST16445 3	96 T C ---			TATAATCCATCCTCCAAACACACACAAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAAATGTTTCTTGATAATGTGGAGAAATCTGCTCTTTAIGTA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	

WI-16879	79 C	GATACAGGC T ATATTCCCA	CAAGGCTTTCT AGAACTAGAGT CC	AGACAGGTCAAAACAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCA/C/TATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCACCCAG
WI-16882	99 A	GAAATGCCA GCGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGGTGGGAGAGACAAATTCCTCCCTTTACCCAAAGGTTACTCTGAC AAGGCTATGAATGAAAATGCCACGTCTCTGAC/A/G/GCGATTACCTGACATGTGTCATCCT
WI-16888	70 G	GCTAACTTTGG GCAGGTTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGGAGAGCAAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC/G/A/TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75 C	ACTTGGCCTGT GTTGTTCA	GTCTATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTGCTCCCAACATCAGAACATAAGTTCCATGAAAACAGGAACCTTTGGCCTGTG TTGTTCA/C/TCCCACTGCCTAGAGAGTATAGACA
WI-16910	74 G	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTTATATTGCTATGACTTTTCATCTCAGAGAGTAAGATGGCG CTAGAA/G/A/GTATCTGTTATAGAAACGATACCTTCAATTTTGGCCTGAACAGTGAAGGT
WI-16918	93 C	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAACTACCACCATCTCTCTGCTACCACAGAGCACTAAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACCAGCAC/C/T/GATGCCACTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A	GGAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTATGGAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGG/C/JCCA CGGGCAATCACATGAGATG
WI-16947a	58 C	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTATGGAATAGGCCTGGAG/C/GIACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43 T	AAATGCACAC TACATAACAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTTACTTTAAAATGCACACTACATAACAACCTAATA/C/JCTTAACTTGGTCCAACCTATTT AGTATAACTAATAAGTTTTTATCTGATACTGATACTGCAATGCCATTAAA
WI-16995	55 T	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGCGGT	TTAGTGCCAGACATCAAGCATAGAAAGAGCAGTAGAGACTGAGGTAATAGTATTT/C/JACGGCTGG AAATCAACATGCCTCTTCTCTGTGAAGTTGTACGATGGAGCTGAGAAGGCTGAGTCAATCT
WI-16992b	60 T	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCACCAAGAGTACACTGTGCGCCCTCATCTGAGAT/G/GTG TAGGACTGTAAGGGAATGTTTGGGGTTTAGGAA
WI-16992a	46 G	AAGCACCAG AAGTACACTG	CACATTCCTT ACAGTCTTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCACCAAGAGTACACTGTG/A/JCCCTCATCTGAGATGTG TAGGACTGTAAGGGAATGTTTGGGGTTTAGGAA

WI-17010	23 T C	TTCACAGGA	AATAATACGGT GTTTTGAATGT CA	ATGTTTCAACAGGAAAGCCATGTC/JATGACATTCAAAACCCGTATTATTAGAGCTCATTTAAT TGTTTAAATGCGACAAAAATCAAGGCTAACTAAAGCAGATCCAATGACCCAGTGATCAACCTAGA GGTCCACG
EST17127 9b	74 C T	CACTCGGCAC AGACAGAGT	GGGAGGGCAGG GGTG	ATCCGTCCTCAACACAGCATCCAGGCCGGCATCTCCCCCAGGATTTTATAATACATCGGCACAGA CAGAGTC/JTJGGAGCCATGGGGCACCCCTGCCCTCCCCAGGCTTCCTAAGTAACAAC
WI-17040	94 T C A	AATTCTCTTAT CATCTCAAGCC	GGACTATGGCT TATTCAGTGAT G	CACGCGTTCAATTAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC GAGAATTCCTTTATCATCTCAAGCCAGTC/JCATCACTGAATAAGCCATAGTCCCAGTCTCGTTTTCC AAATCTTTCTCATATTGT
WI-17044	47 G T G	GCCAAGGGAT TAACGTATAG	GGGGATCCCT TGTTAAGA	TTGTTTTGTTTTGTTTTCTCTCTCTGCCAAGGGATTAAAGTATAGGTC/JTCTTAAACAAGGGGATC CCCCACTTATAGCTGACAGCAGCAGCTGCAACCAGTCACTGACTCTCTCTGAGATGGCAGGGAATCGAAT CAAAAAGAAAGCAAGTG
WI-17021	62 T A ACTC	TGGACTTGTC GCCTATAACT	TGTAGAGTTAG TGGCAGCTGC	GCATGTGTTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTACGCCTATAACTACTCT[A/G] CAGCTGCCACTAACTCTACAGGCACAGTAACACTACTTATACAGGAGCAGATGCCAAAAGTGCCTGG GAGGTGCCAATAAATCAA
WI-17065	90 T C CTT	CCAGAAAGGA AAAGCATAAA	CCCAAGAGAC AATGAAATCCT	TGTAAAAATGTAGACATGGGGGAAAAAACATTCGTAAATCAACATGTGCTGTTTTCTACTTCCGGTA CCAGAAAGGAAAGCATAAACTTT/JAGGATTTCAATTGCTCTTGGGT
WI-17066	32 A C T	TGTACAGCCA ACATCACTGT	GAGATGTTGAA AATGTTCTGGA A	TTCATAAGGTTGTACAGCCAACATCACTGTTT[A/C]ATTCCAGAACATTTTCAACATCTCAAAAAGA AACTCTGCACCCATTAGCAGTCATCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86 T G ...		...	TGCTGACTGTCAATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCAACTGTTCCAAGCAT AACCTCCTACACAGGCCTT/JGCTACATAGGAGTATATTTGGCCAAAGACTCACCAGTGAAGTGAAT
WI-17104b	108 T C ...		...	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCCCTGATGCTTTGCCAGGCTTCCCATTCATTCCA AATCAGAAAGCAGTCAGTGGCCCGTGGTTCCAGACGGCTT/JCTCTTTTGAAGAAATTA
WI-17114a	37 T C	TTCCATCAAG GACTTTGTTT	TTGTATTATAA ATAGCAGAGTG AAGAGAC	AGCGTCCAACAGAGATGTTCCATCAAGGACTTTGTTTTT/JGCTCTTTCACTCTGCTATTTATAATAC AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAAGAGAGACTGCAGCCACAATCAGAGTTACAT GGGA
WI-17150	76 T G CTT	GATGAAATTC AGATAGTCTTC	TTCTCAGAATC CTGGAAGATAT G	CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAATTCAGATAGTC TTCTCTTT/JGCTATATCTCCAGGATCTGAGAGGGCCCTCTTTGTCTGCTCTAATTT
WI-17163	43 A G TAACGTT	CATTTCTTTGT AAAATAACAA	CAGAATCTTGC TTTTGCCTT	GAAATCGAATACGTCCTATTCTTTGTAAAAAATAACAATAACGTTT[A/G]AAGGCCAAAAGCAAGATTCTG TAAACCAACATTTGAAAAGGGGACACAGGGGAGGGGAGGGAAGGGCCAGATTTTCAACGGTTT CCTCCACATCTGCAGACAAA



WI-17178	127 T C	GGACTCCCTCA TGAGGAGC	CCCTCAATTTT CAACTGCTTC	AGCAAATGTCCTCCCAATTTTCATTAGCTATGATGGAGTTATCAGTTTCATTTCAGAGGGAATTACTGG GGCGAGGGGGTTTAATATCTGATGGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA GCAGTTGAAATTTGAGGG
WI-17180b	81 C G	---	---	TCATGGACATCCTGAAGGAGACACAAAAATATAGAGAAATCCTGCACATTCCTCAAGTCTCGTCGACAG GCTTCAACAAATTAC/C/GJAACATCTTGCCCATTTTGTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17180a	47 T C	CACAAAAATA TAGAGAAATCC TGCA	TGGGACGAGAC TTGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATTCCTCAAGTCTCGTCGCA CAGGCTTCAACAATTTACCAACATCTTGCCCATTTTGTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17156	54 G C	TGTTCTCTAAA CTTTAGATATC TCCCA	CAAGAAATAT ATATTTGATTC TGTGGAA	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATTC/C/JTCCACAGA ATCAAAATATATATTTCTTGTTGGAAATTTAAATGTTCTTAACATATCTGCCTACCATCCACCTCAAT TAATATCTTG
WI-17149b	79 T C	---	---	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA ACCCAATTTGTCATTC/GTGTATGAACACTACAAAAAGGATGGGGAAGAAACACATTTCTCTACA CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATTC/JTTCATGCACGTGCGTG GAAACCCAAATTTGTCATGTGTATGAACACTACAAAGGATGGGGAAGAAACACATTTCTCTACA
WI-17197	67 G A	GCAGAAGTAG CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTGCTATGTTGCCCTGGGCTGGACTCCAGCAATCCTCCTGCTCAGCAGAAAGTAGCTGGGGCTAC/G /AJGGTATGCACCACCTCACCTGCTTATCAGTTTCGTTTAAATAGAAATATTTGACTTTTAGATGCGCA TGATTTTCAGTACTTTTCTCCCTGTCCTAGTTTTC/JTAAATTTCTCAGTGGACAAATGGACAA ACCATCTGTTTGAATTTGAAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC TTC
WI-17198 EST18753 8	38 A C 27 C T	CCTAGTTT CTACCCAGGCT GGTCTCAT	ACTGAGAAATT GGATCGCATGA GCTGA	TCGCTATGCTACCCAGGCTGGTCTCATTC/JTTCAGGCTCATGCGATCCTCCTGCTCAGTGGCTGG GATAAGACACAACCTGCCACCGGCTGCCCTAGGAGTAGTCTTAATGCCGTGATGGTGGG
WI-17108b	74 C T	GCCATTCAGTC TCAAAAGTAA CA	AACTACGATTT ATCATATGCTC CC	TTATTTTAAACATAAACAGATGCACCTTGGTTTTTACATTTCTGTTGCCATTGAGTCTCAAGT AAACAC/C/JTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCATTACAGAGT ACACAAAAATTTACCATCGTACCATTAAAGGGTATAGTTCA/C/JGTGGCATTAAAGTACATTTCAACT TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCTCCGTT
EST19067 2b	41 A G	---	---	ACACAAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTTC/C/JAGTGGCATTAAAGTACATTTCAACT TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCTCCGTT
EST19067 2a	40 A C	CGTGACCATT AAGGGTATAG TTC	AAAAGTTGAA TGTACTTAATG CCA	CTGTTCTCAGAGATGACACTGCCAACA/C/JTTCACAGATTTGACATACAATACAGTTATGTATTGGC TATTCACAAATTACAGTAGTGTGTTTTCTCTGAAAAA
EST19125 8	28 A G	---	---	

EST20824 8	115	T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCGGA	GTGTGGAAGCCGGAGTTTATTATTATTCAAATCAGTCTCTCTGAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGGTAGAGGGGCCAGTAAGTCGGGAGTGGCTGATTG[T/G]TCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50	A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCT[A/G]GTAGCACAAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA
EST21904 b	128	G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGTCTGGGAGCAGGTGGGCGAGTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTCATATGGCCATTTTAATAAGTG[G/A]TA TGCTTCTGAACACCTGCC
EST22111 3	82	T C	GAAGATCTGT CTGGCATTTCT	TGGAATAAACA GCCCCAC	CAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATTTCTT[C/G]GTGGGGCTGTTTTTCCAAAGGCACA
EST22197 2	78	T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGGGT	GTTTAATGATCACTCACCAAAATCCACAGGAGAAATCTTAAATGTTTACAAGCACCAATTAATCTGCT ATTCTGCCATT[C/G]ACCGCATCCTTCATGGTAGAGTATCACAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92	T C	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCAATGGTTTTACTCTA[T/C]GTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACITTCATCATCCAG
EST22311 9b	54	A G	---	---	TTTTCCATGGATTAGATCATCTTTTTATTGAGTTATAATATACATAAAAAATCC[A/G]CCACTGTAAA CAGTAGCATTCAATGGTTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACITTCATCATCCAG
EST22311 9a	41	T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TCGAGGAGCTCTGAGGAGC[A/C]ACCAAGGGACGTGTGCCAGGGCCACCGTGCAGGCAAGTGTG GTCCAACTCCTTCCCTTTACAAAACTCCAGCCTACCCACACAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTTTAACTGT
EST22319	19	A C	---	---	GATGTTAATGACTTTCTTTTGAGATATGATGAAAAATATCCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTACC[A/G]TCTGTCAAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22433 c	103	A G	AAGACATGTT CACCAAGTGA AA	CAGCTTCAGCT TAACTGACAGA AGTTTCAGTTT	TATCCATTTCAAGAAAAAATGACTTAAAAAATACAAATCTATCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAAAAATTCATGCAAACTGAAACTATGCTTT
EST22657 9	71	A G	AAATGGATCC TTATCTGCACAT	GCATGAATTTT	

EST22993 5b	71	T C	ATCCTTTTGT TCTACCCC	TTGCGTGTAA TTTGACTGTAA TG	GCCTTTTATTGCTCCTTTTAAACATCAAAATGTTTTATAACACACTTGATCCTTTTGTCTTCTACCCCA ATT/C/CATTACAGTCAAAATTACAGGCAATATAATAGGCTAACAGAAATGCTTGCAATTT
EST23021 0	108	T A	---	---	TTATTTCAGCTACCAATTTGTGTACTATATCTCTGACAAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTATTAAATCTTTGCCCTT/C/ATAGGTTTTTGACAGTTTGTGTCTTTCT T
WI-17387	55	C G	CCTTTCAGAT TGAAGAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTAACATGCAAGTTTCATTTACATTTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAAATCTTAGGCAAAAGCCATTTCTTTG
EST23669 1	101	A C	AATGTAAGCT CCAGAGGCAG	OCCTCCCTCC TGTAAGC	TTTTTGGCTTGCTGCAGAAATAGATGAAGAGAGAAAAATATACCCAGATACCTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAGCTCCAGAGGCAG/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGTGCTCACTG
EST23733 9	31	T G	GGCTGTAGTT TTGTTTTGTT	TGCACCTTTAA TCCCATCAAT	AAAGCTGTAGTTTGTGTTTTTCTT/C/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAGTCCAAAGGCTAGAGAAAGATATGAGGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAA
WI-17470	83	A G	GTCCCGTCCCG CCAG	CCAGTGACGAG GCGA	CTGACACGTCCCTGTGCGGGGGTGCATGTGCGGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCT/C/GJTGCGCTCGTCACTGGCCTTGGTCACTTTGTATTTCTGTCTTGGTTGGAA TACCATCAGCCTTCC
WI-17519	55	T C	GTGTCCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAAATGCATTTGTCTCTAGCTAATGAATGCAT/CJAGAGTATTG CCTGCAAAATATAAATTGAGATTCTATTTTAAAGAGCTTAGAAGACATGATGGTGCATAG
EST25356 3b	95	C G	---	---	TCCTTGATACAGGTAACCAAGTTTGTAAACATTTTCAAGCTTCACTGTATCTTCAAGTTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GJATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26	A C	---	---	TCCTTGATACAGGTAACCAAGTTTGTGTAACATTTTGTACATTTATTCAGAACTTCACTGTATCTTCAAGTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99	C T	---	---	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGTATAATGATAGAACCCAA/C/JTAGGCGCAATTTACATTTGACGCGTCATGC
WI-17581b	86	T C	ATTCAACATT ACTACCAGTT ATTGCGCT	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGTATAAT/C/GATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86	A G	ACTTCCCTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAGGCCTACT TCCCTGTGTAACACTCC/C/GJATATTGTGCGATTTCTAGCTATAAGAAATGGGCGCACTAAGTGGGTC

WI-17623	46 T C ---			---	TGTGGTTTAAATTTAAATTTCCCATATAATTAATGGTGGGCACATTTC/GCATGTGCTTACTGGGTC ATT CATATATCTTTTGGAAGCATCTGCTCCAATCTTTTGCTGACTTTGGAGTTTTTTGGT
EST26419 1b	46 T C ---			---	ATTTACATACAGAGATACAAAGCAACTATGTGCAGCAACAATCTGATTC/GJGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35 C A AG	ATACAAAGGC AACTATGTGC		CAAGAAGTTTG GACTGOOC	ATTTACATACAGAGATACAAAGGCAACTATGTGCAGC/AJAAACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTAAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780	69 G C ---			---	TCAGCTTTAATTTAAGGGACATGTAATAAAGATGCAATTTGACAGGACAGCAGACTAGTTCAAGC AG/GC/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTGCTCGTTTCCATCTTGGCTTTACCA CACTTACAACTGATACCC
EST26900	39 A G ---			---	TACTTCAGTTTAAGGCAAAATCCACACAGAGACTGTCTC/A/GJGAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCACCATGTCATGACGGGAAGCAGAG
EST27152	101 C T ---			---	CAAAGGATTTATTTTGTCCCTAAAGTAATAATCTAGAAAATAGCAACCCACTGCAAGAAAGAGTT CTATACATAAACATTTTCAATCATCTCTCTCTC/JTTTACATGGTGTACTCTTTTCATGTACACAT CATCGGAAAACAGACTGA
EST27504 0a	33 G A ATTT	GCACTTTGCAA CAATTTAATA	GCTGGTGTGAT GCTACTGTAAT G		TTTTGCACCTTTCACAAATTTAATAATTTATC/G/AJCATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGCTTTTCAGTATTTCTGTACACATCTGTAAACAAGAACCCATACATT GGTAAATTCATTCT
EST27662	51 C T CTCCAGTCTG	CACATTCTGTT CTCCAGTCTG	TTATGGAATG GCTTATGTAAC C		ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTCTCCAGTCTTG/JAGGTTACATAAG CCATTTCCATAAATTCATAGCCTTCTTCTTAGAGTAACACACACACTCTGTTTAGGAATGTTT
EST27788	100 A G ---			---	ATTTTATTAGGCGGTACAATTCCAAGGTGGTAAGGGTGAAGGAAAGGCGAAGGCGAGGCAATACAT TATTGAGCTGAAAACAACCTTACATTTCAAGGAC/A/GJGCTTCCAGACAAGCCATGTAGAACCAGCAT GCCITGGGACTGTGTGGAT
EST27828	58 G A AGAACCCAC	GGAAGTCATC AGAACCCAC	GTGCAGAGAGG TACTCCAAGTA C		TCCTTAAACCTTCTCTGTGGATCCCAAGTACGAGTGGGAGTATCAGAACCCCACTG/AJGTACTT GGAGTACCTCTCTGACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAATTC AATCTGTCAC ACAATC	TCAAGAAGGCC TTATCCATT		TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACAATC/G/AJAAATG GATAAGGCCCTCTTGACAAATTTTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTAT/CJAAAAGAAATGATCAATCCCTGTTGCCTCT AAGTCAATGGAATGAAGAGCTGTGTCAGGGACACACACCCGCTGCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG
EST28036	37 T C ---			---	

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTTCTCGCATT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTTCTTCTTTAAAT/AJATGGTATAAAAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACAACAGACGAAGACATGAGTTTGTTCTGACTGTGACACATTGGGTGAAA
WI-17724	50 T C	TGGGOCCTCC TGTC	TGGGTTGGCAG TGTC	AGAAATGGTCTAGTAATCGTTCCAGGATTCGGTGATGGGCCCTCCCTGTCT/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTGTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGTATAGTTACATCATACCAAGTGTACATACTG TT/CJACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTAGTGTGTC
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGTATTA/CJGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTAGTGTGCA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAACACACATTAAGCATCATTTGTCACCT/GA/GCTAACTCCT CAAATCAACAATACCCCTTATTTTAGCCATGAAAAC
EST29128 4	58 A G	---	---	CTTTAGAAGGACACCAGTCTGTTGGACTTAGGGCCTACCCCTATTCAGCAGGTGCC/A/GJTTATTT TCACITGGTTACGTCGTGAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCTTCTG T	ATTATTAGGTAATCTGCTGTTGGGGTGGGTGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT/CJACAGAAGAAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATAAATCTTAAAAGTTAACTCACCATGAAA TTTAAACCTTCTGTAAGTGGCTTCACTGATGAGGCAGTAACTACATAGGGATAAA/GCJAGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99 A G	---	---	AAATAAATACATCATGCGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTAATAATTC/CJAGGATTTAATTTCTTCTAGTTCAATCTTTGGGA GG
WI-16260b	86 G A	---	---	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAAGAAAGACCCAGA GTTTCACAATATAGTAGC/GA/ATAACACAGGCTCACCTTCCCTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAAGAAAGACCCAGA AGAGTTTCACAATATAGTAGGATACCAAGGCTCACCTTCCCTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTTCTTG/GA/GCCTGTTTCTTATACCCCAATATCATAAGAATT GTTGTGCTTCTATATGTTTCAGCTTCAAAATCTTTTGCTTAATCAATCCAAATGAATTACCTGAATT TTCTCCTCTTGTTCAAAA

EST31951 4	87	C T	GGGTTGTCCAG CCAACA	CCCACCAAAAT CACTCC	ACAGCCATTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTTGTCCAGCCCAACA/C/TTGGAGGTGATTTTGGTGGGAATCTTATCACAAATTATTCT
EST31968 8b	95	T G ---		---	CGAATTTGTCTCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGCGGGTTACTATAAGT GCAATTTTATAATGGGATTTCTGCTT/G/AACTGCCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST31968 8a	75	T C T	GCGGGTTACTA TAAGTGCAATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGTCTCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGCGGGTTACTATAAGT GCAATTTT/C/ATAATGGGATTTTCTGCTTAAGTCCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST32063 2	103	C T ---		---	TCCATGGATGAACAGACGCTACCATGCCACATCCCACCTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TTGTTCAAGGCCCATTTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G ---		---	AAGGCTTCCAAGCATTCAAAGGCACTTGGGTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCC/A/G TTCTGTATTAGGAGACACCCCAAGCCAGTAACAATATGGTTCTTGCAAG
WI-17800	29	C G GAGAAACTCA	GGGAGCACAA T	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/C/G/AAAGACTGGGATTAATTGTAGGAAATATTTTCACAG TTTCCACAAGTCAGAAGAGCTAATCCCAACCCCTCTGTATCTGGAACATACACTGCTGCCATTTCTGCG CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCTTCTTAAAGTCTGGGATGACTTTCC/T/G/ATTCATCAAGTAGAACCTAAGCCAAAT TCAGAAATCAGAAATCCTTTTGTCCATCAAAATCCAGCTAACTCAAGCTGAATTAATGTTTCATTCT GTATCTGATGTAGTTAACCATGGCCTGTCATGATTAATTGCTATAAGGAAGGGAACAAATCTTTA TAGTGCCAAAGATAATTAATCTTGGTTTAAATCTTTGCCAGCAAAAGCAAAATAT/AJCCGACTGAC TGCTCTTAGTCTGATC
WI-17860	121	T A AGCAAATA	TTTGCCAGCAA A	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATTTGT/A/TTTGTGTGATTAGTGACAACG GGGAAATCTACAATGCTCAGATCACAGTAACACTAGCA
WI-17866	43	A T ATTGT		A	GAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCATGATC AATCGCCACGAGA/G/AJACTGGATGCCAAAGAGATGG
EST33301 4c	80	G A ---		---	GAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCAT[G/A] ATCAATCGCCAGAGACTGGATGCCAAAGAGATGG
EST33301 4b	63	G A ---		---	
EST33460 1	44	G A C A	AGCGTGGTTTT CAATACTAAA	CTGTATTATT GTTAAATATTT GCATTGT	CTATCCAAAGATATTTATTGCAGCGTGGTTTCAATACTAAACA[G/A]GTGTAACAATGCAAAATATT TAACAATAATACAGTGATTAATAAGCCATGGCATAATCCAGTTGATGTAATACTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAAATAAAATGAACAC[AG]TACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACAAATGA
EST34149 5	69 A G A T	TGCCAAATAC TCAAGTGTGA GAT	AAGTACTAGCG AGAACAACTA ATAAAATC	GTITTTTCTTTGAGTGACACAAGCTTGTTCAATTTTGAGAAATGTGTGCCAAATACTCAAGTGTGAA T[AG]GATTATTAAGTTGTTCTCGCTAGTAGTTTGGTATTTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A	---	---	TGGGAAACATAAGTTAACTCAAGAATATATCCAGTCTTTATGTTACTAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT[C/A]TACAAAGATTAAAGAAACCTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATAAAT CCTAAAGC	CAGAAATTATG TGATAATAACT CCTTC	GGTACACAATTTTAAATGGAGGAACACACAGGTATGTTGAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATACTCTCTAAAGC[C/T]GGAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAATTTTCATCA
WI-17993	118 A C	---	---	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATTATGATAAAACACCTCTCATTTGTGA AAAAACAGCTAAGGGTGACATCTCCAGACCACCAACCACTGTCCCTGTAATGTTA/C]CTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17996	84 A G	GTAGAGCGA AGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGGAGCAGCATGAAACAAACATCTCCCAGGCCCTCGCAGT AGAGGCGAAGGGAACAG[AG]GCTGCCCATGTGCCTGTCTCTAAAGACGCCACCCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33 C G	---	---	ATTCTTTATAAAACACCATGTCCCTAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT
WI-18041 EST35164 8a	24 A C 57 A G	---	CCCTCTGGATT CTGAATCTCAA	GCCACTGAAAAAAGGTGCTCTTCC[AG]GTTTCTAACTCCCTGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAAATACTTAATCA
WI-18052b	67 A G	---	---	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCC[AG]CTTGA GATTCAGAAATCCAGAGGGTCTCAGTCTGTTAGTGTCTCTGTGACATTTCTCTTTG
WI-18052a	50 T C A T C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATC/T]TGGTTACACATCTT A/G]ACAGCAGAGCTGCCTGAGGAGGGTGTGTTTAAATGCTGATGCTCAGCAGAGTGTGCTGGC ATGCCCCATCCATGCTTT
WI-18054	46 G A G A G A T A A A	GGGAGTGGG GAGTAAA	CGTACCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAA[AG]TGAAGCAGGGTGAAGC CATGCAGGAGTCCAGACAAAAGACGGGTGATTTTGTCTCAGGTGGTAGCAACAGAGGTAATG

WI-18064	54 G A	GTAGCTGCTA AGCTGTATTTG	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCTGTGGGTAGCTGCTAAGCTGTATTTTCAGATG/GA/GAATGTACAC AATCATACCACCTGGGGAGAAAGAGTAAGCACAGTGTCTATTAGGTGCCAAACTGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	CCCTGGGCAAC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGGTGGAAATTTTGATATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT/C/JAGCAGGTGCCGAGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C GTGTAT	AACCCACTAG TTACTCAGAGT	AAAACTAATA AGAAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT/C/JATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATAGTTTGATATTTCTGTACTCAGAACATTTTAGGTGCAAAAGGATATAA
WI-18080c	80 C T ---		---	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCCGTG TTTGACTTTTATC/TJCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGGTAT
WI-18080b	65 G A ---		---	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATACTACTATGCCG/G/ AJGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGGTAT
WI-18080a	41 T C AGTCTCTC	GCAAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTC/T/CJTGTAAATTAATACTACTATGC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGGTAT
WI-18086	63 G A ---		---	GTGGGCATCCTATAAAGCAGCCATGTGTTGAAACAAATGATATGCACAGAAAGCATCTTCT/G/A/ TGGCTTTGTTACACGGTTTCTTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTTGAA
WI-18115b	71 C T ---		---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGTAACCTTTGGTATTCOC TTG/C/TJTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCAATACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70 C T TT	TTAGTGTACCT TTGGTATTCOC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAGCCCTTAGTGTAACCTTTGGTATTCOC TTG/C/TJTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATACAATGTAAAGAAAGGGTGAG TCAGT
WI-18136	78 A G ---		---	TTTTGAGAAGCACTCTGTAAAGCAAGGATGCATTCAAAAAATGGCTTTGAGGATTAACTTCTCTCTTA GGTAAATTTGC/JAG/JTAAGAACATAAAGCATTTTAAAGTCCACTGCCGCCTTAGAAACT
WI-18169	115 A G GAAGCTC	CCATCTTTCCG	GAGTCTGCTT GTGCTCA	GGCAAATATTTTACATCAGACCTGGAATCTGCCCAAGTCTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTCCGGAAGTCTG/JGJTGAGCACAAGCAGA ACTCGGTGGGTAGAGTGA
WI-18190b	26 G A ---		---	TGAAAGAAAGTCGACACAGCGGACACTG/JATCAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAATCCTGGCGA



WI-18190	62 G A ---		---		TGAAAGAAGTCGACACAGCGGACACTGTCTAAGTGAACAAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGACATTAAATCCTGGGGA
WI-18181	100 A C CAGATC	AAATATATAC AACACTCCCTT	CGTTTACCAT TTGTTAAGCTT TTG		GACAGTGAAAAACATTGAAACACAAATACAAACAAACATTAGGAACAAGAAATGTGTAATCCAA TGTTGAAAAATATATACAACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAAACGTA TGTTCTTGAAC
WI-18215	78 G A CTGCOCTC	AGCAGAGTTC	CCTCCCTCTCT OOOOC		ATTACATACAGCATTTCTGAGTACAAACTAGGGGACAGGTATTTACAAAAACAATAGAGCAGA GTTCCCTGCCCTC[G/A]GTGTGGGGGAGACAGGGGATTCAGCATTTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60 T A AA	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGT C		CATTTCCGAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAG[T/A]GAA CCCCTGAAAACCTTTATTTTGAATGAAGTTTTCCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C ACA	GGAAACTTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT GAGACA		TTTAAATGCTTAGATTTTCCCTCAGTATTTTATCAATAGTGTGTAAGCTGGAAACCTTGAGTTTGAG ATCACAAT[A/C]CTGTCTCAGTAGTCTATTACCTTCTGTGGGCATTTCGGCAGAAGTGGC
WI-18242	30 G A AATCGTAACA	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAAACAG CTTTC		AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAAT TGGATGCCACAACCTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGGCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119 C T ---		---		GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[A/C]TACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C ---		---		GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T TTCAAA	AAATAGGAAA TATGGACTATC	TTTCATGCATCA TTTGTGCA		GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G AA	GCTGTCAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA		CTGAGCCTCTTGATATGTGGTTTAGTGTCTATCATTAATTTTGGAAAGCTGCAGCTATTGTTATTTC AAAT[A/G]TATCTCTGCTCCCTTTTCTCCTTTTCTGGGATTCATTCGCGATGTGTTATA
WI-18330b	66 A G ---		---		AAACATCTACAGCTGCTTAGGCCATCCTGTGAAGAAATCAGGGGATGAAGAGCTGAGGAACAAGAGGG[ A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTGTGTTGAT TCACA

WI-18330a	49	GA	AAGA	TCCTGTAAGA AATCAGGGAT	AGTCCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAATAAAGAACAATAATTTTGTGGAT TCACA
EST37564 5	85	T	CAGA	AAATTCAAGC CATCTACAAA	CTATGGAGGOC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGGTTAGAACTACTGCATGTTATTTAAGCTAAAATTC AAGGCATCTACAAAAGATT[C/T]CTCATTGAGGCCTCCATAGGCTGCAAAACACATCAAGGCATTAC TGTAAGTTAGGAGGAGGACTGAG
WI-18327	104	GA	TT	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAAGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGCGAGTTCCCAAAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	GA	---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCA[C/T]GCTGA CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	CT	---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCA[C/T]GCTGA TGCCCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGTTTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	C	GCA	CCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTCTACCGTGTGAGTGCCATGAAGCCAAAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCA[C/G]TCATCTTCAGTCTTTGAGTCTTCCAGCCCCAGGTCCAAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	A	G---	---	---	TTTTATCTGGTCAGCTCCTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTT[C/G]ATGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	GA	---	---	---	TTTTATCTGGTCAGCTCCTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTT[C/G]ATGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	CT	CCCT	GCCACTTTGC CCCT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGTCAGCTCCTCTTAATGGCCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTGAAG AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTT[C/G]ATGAAGTGTTCCTGATACA GCTGACGTTTCGAGGG
WI-18012b	46	T	C---	---	---	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCAATTG[G/A]GTAATTAAGTTTATTAAATCAGCTGACTTAGCATTTGGGAGATTATCTGGAT
EST38390 4	75	A	GCTG	GCAAAAAGGA CTGATTAATAA	GCTAAAGTCAG CTGATTAATAA ACTTAA	

EST38512 7	91 T G	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAACTGACCCCAATTGGTAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAT ACCTGATGACGATGCCAATACTTCGTTGJGCTCCAGAGTGCAGTGAATAACTGTTATAGCC CCTGCACCTCTCTAAAGATCTTTTC/TTCCCCCAAGTCTTAACAGAATGGTATATCTCTCTGGA AGATGAACGTCATCAATGGATTGTGCTGCTCTCGTTTTCAGCTTTGATTTTTTGTCTTGAGAACCTTG TCCTCCCTGCTGAATTT
EST38519 0	24 C T T	GAACATCCCA TGTTCTGTTT	TCTGTTAGGAC TTGGGGA	AGTGGTCAAAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTCTGTTTAAJ T/CJTCCTTATGTGTATATACTACCTTCCCTTTCTCTTTATACACATAGATTTTCCCTTAATTGCAGC CCA
EST38575 1	66 T C A A	CCTGCTOOGCC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGAGGCTACCTGAGCTCTCTGTGCTCCACAGAGTGGGTGCCTCAGCCCGGGGCCCGGTGG AGTCTCGCGGGCCCGCCCTGCTCCGCCCTTC/GJGCCACCATCCAATCTCCAGGGG
EST38616 9	101 C G C T T C	TCTGAACTGGG CATTTCAA	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTCTCTGCTGCAGCAGGAATTAATTCAGTCTGAACCTGGGCATTTCAA[T/C]GCGGTG GTATTTTTTCTTTCATTTTTTGCAAGTAAAAAATCAT
EST38652 8	59 T C	AATGGTCATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATA[T/C]AGATAGAAGATTAAAGGACCAT CACTGAGGTCACATAGCTCAGAGGAGAGTTAAGATTGGACCCAGGAGTTGGTTCCAGCATATA
EST38654 5	42 T C	GTTTTACA	ATC	GGATCCTCACTCACTGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCCGJAGJAGGCCAGCGGATGTGTGCCCTCTCTCCCAACTCATCTTTTCAGGAACACGAGG ATTCTGCTTTCTGGAAA
EST38707 9	75 A G ---		---	TGACCTTGATTTCTTCACTAGAGGGGAGAAGAAATCACTACCTACCTTTTGGATGCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGGJAGJCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAATCTTTGCC TAGCAGCACCC
EST38759 2	86 A G	TGCTCCCTGA GGTGATATGG	TCACCATCGTG GACTTAAGG	GACTCTCAACCAAGAGAAAAATCAATAGGAGAGGATTGGCT/JATTTGAATTCAGAGCAAGCCCT CTTACTGAGAGGTGAGCCCGAGCCCTCCAAATGCCCTTTTCATGATGATTAGGATCTCTAAGTGGTAC AAACAAACCAACATGGTGG
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTCACTTATGTGTGTTTCATTAACAAG TGTTTATGAGAACCATTACACA[C/A]AAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38815 4	91 C A CA	TGTTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	TCCTTACTGTGCTTACAACCTTCTCTCCAAAGTTTGGGTGTTCCATATTGTTATTGTTATTATTA TTCAACACAGAGTAAAAAGAACTCATGAC[C/T]TCTCTTGGACTCGCTCTCTCCCCAATCTCGAT ACCGACTGCACGTGG
EST38858 4	98 C T TGAC	CACGAGTAAA AAGAAACTCA	GGAGCGAGTCC AAGGAGAA	CCCTAATGGATTTTACAGCTCATCTGAGTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG ATGCT/CJCTGTGTCTCCGTCCTTCCCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGTCTTAGTTGTTAA
EST38865 2	72 T C	GCTGTAGAATT TGTGTCGATGC	GGAAGGACGG AGGACACAG	

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCITCAATAAA TCTCATGTCT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAAT/CJTGAGGACATGAGATTT ATTGAAGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAATTTGAAAACATTTCCC TTATCAATGTCTCATCTCACACATCTTTATTTATTTGTTTTCACACTTCTCAAATATCGGATTTGTC TCATGAGAATAATGGCTGAGGGAGCTGGCAGCGAGTCTCTCA/GC/GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATTCAATGTCTCATCTCACACATCTTTATTTAT/CJTTGTTTTCACTTTCTCAAATATCGGATTTGT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCAGCGAGTCTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTTCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	
EST38909 5	47 A G	GCACAGCATG GCTAAAACG	GGTATTTGTTG ATTCCCATCTT T	GCACTAAACTAACTTTTCATTTGTGGATTGCACAGCATGGCTAAACG/GJTAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT
EST38911 9	85 A G	GTGAGGGAA ACTTATAACCT CAC	TGTTGTTTTGT GAAACAAGCG	AACTGAATGGCAGTGAAACACACTACACATCAAACTTAGGGAAATGTGGTTAGTGTGTACGTTGAG GGAACTTTATAACCTCAC/GJCGCTTGTTCACAAAACACAGCAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C	TGAATTCCTT GGTGG	CACTGCAATCT CACCCCC	TAAACATTOCCATTGAATCCCTTGGTGGG/GC/GGGGGGGGGTGAGATTGCAGTGTCTCAAGATAAA TATCACAATAATATCAAAACTTCAAAATTTGTCTATGCATTCACACACTGACATGAGCCACAAACATT CCITTCACAGGGACTGTAC
EST39002 0	42 G A	GGACCTTGGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCCTGGGAGATCCCGGACCTTCTGGTGACCG/GA/CAGGGCTCCCTGCCAGGGCTGG CCCCTGACCCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCTAAGTTCCGGGTCTCCTCAGTCTGGATGGCTGTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAAT/GJAGGGGCGAGGGGGCGATGCCCGCAGCGAGATGGTCTGTAGGCTGTGGGTC AAAGACCTAACTTCTGGA
WI-16398	90 T C	TCCCTATTAT CCATGATATTT TCA	GAATGGTTTGT GAAAAATATA TTGATAI	AAAGATAATGTCATCACACGCAACATATAGAAACATAAAAGAAAAATAAGTATCCACCCTAAAT CCCTATTATCCATGATATTTTCAAT/CJAGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C	CCTTGTCTC AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGCTTTTCATGATTTTCTCATTTCTCATAGGTTTCTGGTCTTTGCTCTCAATTTTAAACACTT T/CJCTTTTATATAGGGAATTAGCCCTTAAACTGTGGTACATGCTGCCAAAAATTTCTCTCCAGTT
WI-16406	24 C T	GCTTAAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAAA AA	GCTTTAATGGCTACAGAAAGAGG/CJ/GGTTTTATTTCTTTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGCATTTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTTCATGTTTTCATCTGAGAAATAAACCTTCCTGCTGCTAAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAATGAATGAGGTGCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGOC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGTACTATGTTTAAATTGCTGAGCCAGCAACCCCTCGAGTTACCGGCCCTTTACCCCAACGCC AGCTCTGCTTGTCTGCAT
EST39366 2	72 T C	---	---	AGAAAACATTCTGTCTGATCAGAGGAAGATGTATGTAGAAAATCAGAATCTGACTGAATTCCTAAA ATCTATT[C/J]ACACTGAGAGGAAAATGGAAGAAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGGTTTCAGA
EST39371 9	86 A G	CATTGGATTA GCGTGAGAGG TT	TGATTTGAGAC ATTTACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTTATGTGTGTAAATCCAGTTGAGCAITTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAATCAAATGCTTCTCTCTAAAGATTA GACATTGCCCAACCCCTGC
WI-17177	23 A G	---	---	ACAAGTGACATATCCAACCAAC[C/J]TCCATCCCCACCTGTGCCCTATTCTTCTTGTGTTTCTTT AGAGCCTTTTCAGCTATTTCTCTGTAAGCAAACTGCACGAAGGCCCTCCCCGCTACTCCTCCCTGGAA G
EST39428 8	31 C T	GCTCCACACA ATTTTGATT	GGTCCCTTATG AAGCACCC	AGGTTCTGGTTGCTCCCCACAATTTTGATT[C/T]GTTGGCTTCATAAGGGACCCAGGATTCGCAAT TTCTGGTGGGGCCTAGGTAATTTCTGTGCCCTTTGGTCCACAGACACAATTAAGAAGATCAGGTCT GGCTGTTCG
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT C	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAAAGTATGTT[C/J]CAATACCCCGACCCCTGA CCCAGTACCTTTCCCTCAGGCCCCAGGCTCCGGTGGAGGATGTCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA GAGTAA	TCCTGGAAAAC TGACATAAAC C	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAAAATAACAGGAACCTATTATAT ACGTAATACACTTTTCATACCTGCCTACTGACATAGGACTTCAGAGTAAT[C/T]GGTTTATGTCAGT TTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTGGGCC CCTCT	ATGTTGTCATTAGAGGGCCACAGGGGATGGGGAGTAAAAAATAACATAAACGAACGAACAGAAA TGCAGGAGGGTGG[C/J]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCTT GTAGACATCT AACATTAG	CACITGCAATT CTGAAGGCT	TGCTTACAAACCCATAACCATAGGCCATGTGTTTCAGACATTTTGACCAAGCCTAAAGATTCCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAAGTTTCAGTCAAAACCAATTC
WI-18387b	84 A C	---	---	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CATGCTTAGCCATAC[C/J]CATGGTAACATTGACTATGGAGCTTGTGAAAAGTGAATGTGCGATG GCTATGTAGACATAAAGA

WI-18387a	57	A	G	CCTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACAGJTTTGTG GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGCGATG
EST40601	78	A	G	GCGTGGAACTT GAAACAC	TTCTTGAAGA AAGGCGTC	GCTATGTAGACATAAAGA TCCCAGGATGGTTTATCCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGGTGACTGGCGTGGA ACCTGAAACACAGJGACGCTTCTTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32	A	G	AGTGTATCAC ATCTTCAGGAT	GCACACCCCTTC ACACTGTTA	TCCATTCAAGTATCACATCTTCAGGATAGGTJAGJATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTGA
EST43091	28	C	T	CATTCTGGTCT TTATTTTGGGA	AAACTGATTT GTTAAACATG	ATGTCATTCTGGTCTTTATTTTGGACACJCTJTAGCATGTTTAAACAAATCAGTTTTCATAGGCAA CCTTTTGAACATCAAAAGAAATACAATATATTTTACAAATTTCTCATCAGTGTAAATTC
WI-18420c	108	T	C	TTCCATTAAAC AGGAAGTTTC	AAATCTCAGC ATTGCTATAAG	AGAGACACAACAAGAAGAAATAGGGAAATGGGAAGACAGAGTGAATTAAGCAAAATCTTGA TTCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAJTCJGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38	C	T	GAATAAGGGA AAATGGGAAG	CCAAGATTTC TTTAATTTTCAC	AGAGAGACAACAAGAAGAAATAGGGAAATGGGAAGACJCTJAGAGTGAATTAAGCAAAATCTT GGATTTCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101	T	C	--- CACCTGTCTCT AGACAGATTTC	--- CCTCCTGTTGT TGTGTGCA	AGCTGATCAGCTGTCTGTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC CTAGACAGATTCAJCTGCACACAACAACAGGAGGTTCJGGGGTGCACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81	A	C	A CCTTTGGCTCT	GTATCCAGA	AAATTGAGGTCCGGTGGAACTATAAAAGGAAAGAAAGAGAAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTTCCAGTTCCTTCTTTGGCTCTAAGTGGGACTA[CJ]TC TGGATACAGTCAGGGGAG
WI-18449	129	C	T	AAGTGGGACT	---	ATCGCTTCATTGAAGCCTGCTTAATTCTCTCAGTCAACTGGTGGCCCCCAAGACATATTTTATTCTT AAATGTCCAATATCTGCCTGATGTCTGTGTTGTGCACATTGGGGCCACAGTTCJAAATAGGCTAAA AGGCAGTCCACCTGCT
WI-18457	120	T	C	--- CCACAATGGC	TTTAGGCTTTG	GGTGTATAGTGTGTACACCACAATGGCAGAGGTGAJGJTAGAAACCATCTCAAGCCCTAAAA TATTTACCATACATCCCTCAGCAAAAGTTTGCTAATCTCGGTTTAGGGACTCCATTGAG
WI-18462	39	A	G	AGAGGTGA	AGATGTTTCT	TGAGGACGTGTGACAAGCTCAGAGGGGTGGGGCCGGCTGAGGGTGGGGTGCAGG[CJ]GGT CACTCCATCTGTGCCCTGGCCGTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT
WI-18476	60	C	T	GAGG	GTGACC	

WI-18491	109	G A	AACAAATGGT AGTGGTATT AATACTATT	CGTGTGCAATT TCITGTAAATCC ACCTTTACACC GOOC	CTAATGAGATGAATACATGGAAGCGGTTTAGCACAGTGCCTAAACACAGTAAGTAACCAACAAT GGTAGGTGGTATTAAATACTATTATTAAATCCAGAATGAC[G/A]GGATTACAAGAAAATGCACA CGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT	GGGGAACCAAC CAGG	AGCCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGCTCCGAGAGCTCGAGGCTGCTCTTTTATAT GTGACGGGC[C/T]GGCGGGTGAAGGGTCAGAGA
WI-17675	103	T C	GGACATTGG CATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAACTAACAATCTTACCAGGTGCTGAAGAAAAGTGTCTCGTTTTAAT TGCCAAAGCAGGGATGGACATTTGGATGGTGACTT[C/C]CTGGGTGGTCCCATAGATTCAACCAT TGCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CAITTTGGTTT TGG	GATTCAATCAT ACAGGGGACTT	GATCCATTACCTAGGGTAAATTTCTCTGAATGTCAACAAAGAGATAAACTACATTTGGGTTTTGG G/TJAAGTCCCTGTAAATGATGAATCAAGAAATCCTCAAGTCTGCTTGCCACCCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAGG TTGGGGA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCCCTGACCCCATGCTCATGGAATAATGTC TTCCACAAAACCCGGTCCCTGGTGCCAAAAGGTTGGGAA[C/G]TGCTGGTCGGTACAAAAAGTAATT G
WI-17690b	79	A G	AGGCATTTTC TAGCTGTGTTT	---	ACAACATGTGAAAGAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[G/G]ATTACAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	G A	AGGCATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTT[G/A] TTTGGCTTCCCTATAGATTACAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCATCCAGATTATTTCTGAAGTGGAAACCCCTCCGACCCAA TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGT[C/T]GAG CTGGATTATTGCCCTCAA
EST51717 a	39	C T	---	---	GATCCAATCTCAGTGTCTAACTCATCATCCAGATTATTTCTGAAGTGGAAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCCTCAA
EST53012	97	C T	TGGTCACTTTG GGGOC	GGCTCTGCOCA GGOC	TTTCCAGGTTGACAGGTTTATTCACCCCTTCCATCCCCCATGGCCACCCAGGCAGGAGGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGCGTGGGAGAGGCGGAGGCTGGTTTACATTCTGT GGGACGGTGTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTACATT TT	AAACTGCAATAAACAACAAAACAGAAGTCCAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCAATGTAC[A/G]AAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	A G	GGAGACCTGC AGAACTTAA GCA	GGCCTTTCTAA CAATAAATGCT C	TTTCGAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTAAACATGAAC ACATTAAGGAGATGGCC

[illegible]



[illegible]

TIGR- A003P30	117 C G ---	---	---	ACAAGTTCAAAGGAGAACTTCTTTGTTTAAATGCAGCTGTGCTCAGAAAGCCTGTGATTTCCCTAGGA AACCATCTGGGTTTAGCCATTAGCCATTAGAAAATGCAGTTTAAAGCAGTGTCA/C/GJACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156 C T A	TTAAA	---	GCTTGCTTTTATGTTAGGTCGGGGAAAGGAGGGCTGACAAACCGCAGACATCTGGACACACAGC AAGGGTCCAGGGAGGTTGCAGAACTCTTTGCTCTGGCTAACAGCTGTCATGTGACAAATAGCCA AACCTCCTCATTCCTATAAA/C/TJCTTTAACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C ---	---	---	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTCAAGGAGATAAAACCAAAATGAT TGAGTATGATAAAGAAATTTTGCATGGCGATT/CJAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA	GCAATGCAAAA TTCTTTATCA	---	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTCAAGGAGATAAAACCAAAATGAT TGA/GJATATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TIGR- A004V08	60 T C GGCAATCTCTT	TCCTCCACAA AAAGGC	---	CCTACAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAAACAGGCATTCCTTA/T/CJGCC TTTTGTGGGAAGGATCAATTTGGTGCATGCACITTAGGGGACAATTTGGGCAGTAGCTGTCAAAATTTG AGTAGCTGTCAAAATTTCAAA
TIGR- A004V26	125 A G ---	---	---	TCCTAGCTATAAGACCAGATTTTAAATATCTAGATATAGAATTATCCAGAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAAATATGCATTATCTTCACATGA/A/GJAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG
TIGR- A004V28 a	29 A G CGATCTC	CGGAGGTGCA GTGAGC	---	CCAGGCTATAATGTTGTGGGTGCGATCTC/A/GJCTCACTGCAACCTCCGCTCCAGGTTCAAGCAA TTCTCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCTAACTAAATTTTGG TATTTTGTAGTAGAGACATTGTATTTTGTAGTAGAGACAGG
TIGR- A004X20	25 T C GA	GAGAC	---	TAAAGTTTCCCTCTCTCTGTAGGA/T/CJGCTCCATGTTACAGTCAACTATAAAACATGGCTCATGT TCACCTCTGGGCTTCGCTTCAGAGGAGTTTGATAATTTTGGAAAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTTCTTTCATTTCTTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCTCT
TIGR- A004X30	26 T C CCAC	CTATTTT	---	TTTTGAAATCTTAGAGTAGAACCCAC/T/CJACTCTAGTAATACTTTGTAATAAAATTAAGTTT AAACACTTCCATAAAGAAATAGGGGTGCCAGCTCCTTGATTTTCCCTTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T GATGCAAAACT	CTTATAATTAG AAATTTTCATGA AAGCAA	---	CACGGTATATGCCTTATATATAGGTATATACAGATCGTACACAATATATTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACTT/GJTTGCTTTCATGAAATTTCTAATTAAAGG ACTGTTGCTTCTTCATATTCATGGACATTACAAAATACAGTCTCTTTAGTATTAGACGCTC TCCTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAGTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGAGAGACAACACTGC AGCATTTTTTCTTTTTC/TCTTCCGATGACCATCTTTTGGCTGGGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTCTTAGTGAGACTGAGGATCTGGTATAAGGAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGAGGTT AGGAGACT	CAGGCTGCGG GTCC	GTCTTAGCAGAGGATAACTTTGAGGGACAGCCCCCAAGGCCAGGTAGCCTTCAGGGGCGGGCA GGGTTGGGGAGGTAGGAGACTCTGGACCCGACGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGCTCTC
TIGR- A005D17 c	81 T C ---		---	TATGGACTGTGTAGAAATATGATTTGGACAAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCT/C/GTCTAGATCTTCTTGGCCTCTCTGTGCAGGATCTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAACTTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG[G/C]CTGCTAGATCTTCTTGGCCTCTCTGTGCAGGATCTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTTAAA CTGTTACAC	TTGCTATTAT TTAAAGCCAA AAAA	CATCAGTAACATATACACAATTTGGTCATCAACTGAACCTTGCCCTCCAATATATTTCTATACAATCTT AACATTATTGAACCTTAAACTGTTACACTG/TCTTTTGGCTTTAAATAATAGACAATGATTTTTTG TCTATTACTTAGTGATAGACAAAGTGATTACTTTGTTAGACAAAGTGATTACTTTGTTAC
TIGR- A005E31b	27 G A ---		---	GGAGTTCAAATTTATAACCAAGGCTCTG/AJCTCACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTTGCCTGCTTGCCCTTACAAAGCCACTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C ---		---	CTCAGTGTAACAACTTTGTTAGGGAAAAAATAATCCAAATGGATATATGGGAAGAGAAGTG CCAGCTGGATGGTGTGAGACAGAAATGACCCCTTGGCTCTTTATTTGTTCTTTTCAACAGGACC CCACAGATATTGCGGTATGTCATGAGGACTGGGATGCTCTATG/CJGGATGCTTCTATT
TIGR- A005E42a	42 A G AGAG	AGTAAGGTTA CTGCACCTTAC	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTTACTGCACCTTACAGAG/GJCTCAATTTCCCTGATTTAGGA AGCGGATGCTAATGGGTATTGCATAGGTGAAGTATAAAATGTTGTATTTAAGAGAAATCCCAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTAAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC/A/GJTACATTACCTCACAGCCAGGTTGGCAATGGTCATTTTGACAAATGGTCATTTTG ACAC
120979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CJTGCTTAGGGTGTCTCCCCACAGAGCAGATACTTTGAACCG ACTCAATCTGTGTAAAGAGCACTTTGTCTGCTTCACGGACCTCCCAAGGTGTCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTTGTAAAAATTCGCCCAAGAGCCGCATATGAATCTGCCC

X57830	106	G C C T	AGTGGAAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAATAATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATATCTG[C]ATGCCTCATTTATTCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGGAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72	T G T G G A T C	CTTTTAAAGAA ATTTTGTGTTA	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTATATTAGCTGCTTTTAAAGAAATTTTGTATTAG GATC[T/G]GATAAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCCCTGGACACTGCAGCTCTTTT CAGTTTTTGCCTTATACACAATTTCATTTTGCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	C T ---		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGCTCTCATCACCAG[C/T]TAGAGCTTCTCCCGAAGGG CCTTAGGATAGGAGAAAGGTTTCATGCACACACGTGTGAGAA TGAAGAGCCCTCCAGACCACT CTACAGCTGCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGTAAAGG TCCA
D28513b	133	A G ---		---	ATGACCAAAGCCACCACATTTAGAACITTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACCTTTGGACATGGCTCACAAGCAGTTTTTATTGACTGCATGAATGC[A G]TGTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G ---		---	CCACTCCATCTCTGATGCCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAA[A/G]TCTCCAAGTATCCTACCTCCCTACCTCCTGACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G ---		---	CCACTCCATCTCTGATGCCCCA[A/G]TATCCACAGCCTCCTTCCCGACCAAGACCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTCCTCAAGTATCCTACCTCCCTACTCCTGACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A ---		---	CTCCCTGCCTCCTCCTCCTGCTGCTGATGCTCCGCTCAAAACAGCCGAAACCTGCTTGCATGGGGG GAGGGGGGCTT[C/G]A/C]TTTCCCTCTCTTGGCTTCTCTTATTCCTCACAACCACTTCTCAATAAA GCCAAAAATCTTCTCTTCTCCCTCCTCAGGCCACCTCCTGCTCCTCCTGCTGCTGCTGCTGCTTTT CTGGA
D37931	64	T C ---		---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAATAGCAGTGAGTAATGCATTTTGAGCTG[T/C] CCCAGGCTCTGTCTCCTCAGCTCATTTCTCTACTCTTTTCTCTATATACTCATCTTATTAAATACATT GCACCAAGAGATATGGAGACATAAACCTGTATGAATGAGGCTGGGCTTTTCTGTAAATAAGCTTCC TTT



EST25476 9	33 GA ---	---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAA[G/A]CTTTCTCCTCCTCTAAAAACCAACACA AGAGGTCTCTTGCTGCCCTTCCATGGAGCTGGCGGCTGTGGACTGGACCGTCTGCTGA
EST26183 2	70 TA ---	---	---	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACCTTTGTAAAGATTGATCTCTAAATAAG ATT[A]ACATCTCGGGTACTCGGGAGTTAGAACAAC
EST27231 1a	28 TC ---	---	---	AGAAAATAAGGTGCTACCAAGAACTCATG[T/C]GATAGCGCTTTCTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTAATCACACACACACTGTGCCCTTAACAACAACACCGGTGACTCTGA
EST27816 5a	26 TC ---	---	---	CAACTCAAGGTACAAAGACAATTGCATT[C]TAACATTGTTATAAATAAAGGAACATCAGATCAAT CATTAAAGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 AT ---	---	---	GTTTAATTGGCGTATGGTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCAAAAGAGAGAGGAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25 AC ---	---	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGTATAGTACTGCATCTAATCTCATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGCTAACTTAAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a	59 CG ---	---	---	AGCTATGGTAGAGCAAAATCCAGTGGTAAATCAAGAACTCTAAAGTTTCAGTAGAGA[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGIGAGG
EST32515 7	25 GA ---	---	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCCTCTAAACCTGTTGAATAGAAATATGGCCAAAT ATTACAGTTCTCAGTTTCCCTATGAATACTGGCACTGTTTATTTATCATGTTTATATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST33274 4	27 TC ---	---	---	TGCTTTGTTCCCTCCAAATCCATAAAAT[C/G]GTGTGTTCTCAAAGAAATTCGTGGAAGGACTTTGAA TACGAGTTTGTACCATATTCGAATATTCGAATACAGGTTTCAGATAACTATGGAGATGATACCAT GGACTAGGTA
EST33352 7b	75 CG ---	---	---	TACACATTATTCAGAGACCACTGACATGCATCTCCTCCGAGATACATTCGTCTCTCTTAGAGA AGTTTA[A/C/G]GCACATAGTATTATTTACTAAGAGAATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126 AC ---	---	---	ATTTTCCCACAGCAGAAGTATTTATTGTGCTGAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACAGTACAGAAATGTTCAACAAAGATTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90 AG ---	---	---	CCTTTGGGGGAGTTTAAAGCCAGAATGTGACAAAAGTCACTTACAGGAAGACTGGAAATGTAGCCATAG TTGAACCTTAACATCGTCTATAG[A/G]ACCATTTCCTCGTCTCCAGTTAGGTTCTAGGCATCTAAGCT GCTC
EST33508 1b	45 CT ---	---	---	AAAAACATGCTATTTGAACAAAACITTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---			AAAAACATGCTATTTGAACAAACCTTTTATAAAGA/A/GJTAAGTTGACTGAAAAGCAGGTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---			ACAACATAGGACTGGTTATCTTGTTTGA AAAATATATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAAAC/C/JJCTTTGAACACTACAGCCTGAATCCCCC
EST34739 3	97 T A ---			GAAGTATCCTTCCCAGTGGCAGGAACCTGAAGACTCCAGATCAACAGGTTGGACCTTTTCGTGATGA GCTGATAGCTTCTAGGCTGTGGGAACCTC/J/AGGTGCCCTTACAACCTCCAACACTACTGCAGAAATTTCT TGTTGTGCCCTCATAACA
EST34792 6b	104 A G ---			ACCTGACTGCTTTAAAAGCTCTTTGTAAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA/A/GJGATTCAGGAATTCCTAGTCCTATTACA AAGATTTGTGCTGTG
EST34835 9b	93 T G ---			GGAAATGTTCCCTTGC AAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTTGTGCTTCTGGT/GJGGCCCTAAAAGAAACAGACAAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---			GGAAATGTTCCCTTGC AAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGTCTATGTTG/JGJGCTTCTGGTGGCCCTAAAAGAAACAGACAAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---			CACAAAGTCCACTTACTTACATGAAGGAACATAAAGGCATGAGAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAAGAGGTTCTC/G/JGCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---			TCCTTTCAAAATTTTGATGTAGGCATTTAATG/C/JTATAAAATTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAAGTTGGGCATGTTGTGTTCCATTTTACTAGTTTCAGAACTTTTTCATTTTCATCT
EST35708 9	32 C T ---			CTGCCCCAAATTAACCTTTAGGCAATGGAA/C/JTAGACTTACTGTATGGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGGTTGGCACCTTTCCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G ---			ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAGGCTCCA/C/JATGTTAAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---			TGGTCCATTATATAAACTGAGGGGAACAAACGGTGTGACATGGCAGACATTTATTCAATGGAGA AGTTCCTCCCATGAACCAAGA/C/JCTTGCTCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAGGCCTGTGA
EST36301 4	93 C T ---			CACCTGTTCAATGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCTAGCCTACAGC AGTCAGGAGGCAGCCATGGCCCCCTG/C/JGCTGATGGAGCTGTAAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---			GCCATCAGCCCCACAAGACATGACTACCAACG/C/JGGCCCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGCTTAGTGTG

EST36620 6	50 G A ---	---	---	GACITTTATTAGATAAGGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAAGG AAGGCTTATTTAAATATGGGAAATAAAATACAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G ---	---	---	CCTGTGATGTCATGGTGCCTGAGCAGTCGTACTTACTATGCTGACAGACTCAGTATGTCAGGA AAGGAAGTCTGGGGATTCTA[C/G]AGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST36729 9	62 C T ---	---	---	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCCTCTCCTCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---	---	---	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A/T]CTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTTACAACCTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	---	GGTCTACTCTCTTGCCAGGACGGTTTGAAACTCTCTGAGCTCAAGTGACOCCTCCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACACCTGGTCTTGGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	---	AATAGTCTATGGCTACGGGCCCCGTGGGATGTTAAAAATTGGGATTTTAAATTAAAGATTGTGAACATG CAACCCAGCAAAATTTCTCAGCTTATATTTTGAAGTCT[G/C]AGGAGAAAAAATGGGGTCC
EST37284 2	93 G T ---	---	---	AAAAGACCTTTCTCAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAAGGAA GCTCTCTGGATAATGTCACTCTAGGAA[G/T]AGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGTGAGGAATA
EST37315 2a	90 A G ---	---	---	AGATGGGGTCTTGTAGCTTGCTCGGGCTGAACCTAAAGATATCTCTCTCCTCAGCCTCCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACCTTCAAGTTTGTGATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACCTT[C/T]AAGGGTGAAAAAGCATACC ATTCCATTTAGTTGAAATATTCCTTCACATAGCCCAACACATTTTTTCAAGGCACTCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	---	GTGACATCATGTCTCTCAATGCCCTTTCAATTAAATAGTAGT[C/T]GAGCGCTGGGGGCTGAAGTCAGACT CTCTGGTTCAAAATCACAGTGTCTGTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGTCACGG
EST37376 8a	41 T C ---	---	---	GTGACATCATGTCTCTCAATGCCCTTTCAATTAAATAGTAGT[C/T]GAGCGCTGGGGGCTGAAGTCAG ACTCTCTGGTTCAAAATCACAGTGTCTGTCTCTGCAGGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG



EST37378 9	63	T G	---	---	ACACACAAAAAATGGTGGCAGAAAAATCTGGAAGATTCTAATAACCTCAATTCGTGAAAAACIT/G JAACATGCCTCAAAAAAGAGGGGAAAAAACTTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46	G A	---	---	AAGACATAAATCTGCAATGAATCAGTTATGAAATATTAAACCTCT/GA/CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAAATCAATGACGTAGAA
EST37613 6	34	A G	---	---	CTAGGCATGGGCTTTTACAGTCATTTATTTACG/G/G/GTCATGAATTCATTAATAAACACACAGCGAT ATAGCAATGAGCAAAACAGACCCTCCCCAAAATCACCCCTGGTTCATGGATCTTCCATTCTAA
EST38025 4	56	T G	---	---	TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTATATCACATT/G/G/TTATCTCA ACAATCTTGAAGGGTGGTATTATTTCCCGTCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57	C T	---	---	TCTACAGGTACCCAAAGTATCTGATATGCTTTAAGTGGCATTTTCATGTACATT/G/CTGCGCATGG AAGAACGCTCTCTTTTAAATCCCTAACTCTCTTCTTCTGGGAAGACAGAACGTCACAA
EST38420 6a	100	T C	---	---	TAAATCAAGGCCTCTTTTATTACCAAAACAAACAAAAAAGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGCATCCTGACTGAC/T/C/GTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATTCTCCTCTCTCA
EST38950 5	25	T C	---	---	TTTATTGCAAAAGTAAGCAGCCGG/T/C/JGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCCCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGGAAACAAAAAGCTT ACAAACAAAGAGCAGCCCA
EST39053 6	90	T C	---	---	TTTTTTGTTACTCTGTAGCCAGTCATTAAATCTGAAGTTTAAATATATCATTTTATTGGGATGAGATCA TAGCTTTTACACAAATGCTATG/T/C/JAAACAAGTTACTGAATATTTTACCTCGTGGAGTTG
EST39331 1	70	G C	---	---	TCCTCTTGCTCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCCATGGAAGGAAAGTA TGC/G/C/GTGTTTTAGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31	C A	---	---	GTCAACATTGACCTTACATAGTGCCCTCTAGT/C/AJACCTATGAGGCCTAGAACCTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37	T C	---	---	TTCTAATAGCATGCCCTGTGACAGGGAAACTAAGCTC/T/C/JCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCTTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTT AATAATCTGTTGGGACTCA
EST40549 1	42	A G	---	---	TGTTTCTCTAGAGAACCCCTGTGTGATACACTACGATCGACA/G/JATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACCATTTCTCACTTTTGAACCTAGCTCCCTGCAAAAGCACCTTCTA CCCTGCACTTTTGGGAG
EST40579 1	81	A C	---	---	TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCACTTCTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA/A/C/JGGACTTGGAGACAGCGATTAAATACGGAACAGGCTCTCCAGGAAG TTGTATGGTTGTAGGAATTTGGGAAGAAATATCTGTGAAGGAAATTTGCCACTGTGTAATGCACACCC A/G/TTCTGTACTCCCAATATCTCTATGTTTAAAGCT
EST40584 3	68	A/G	---	---	

EST51340	51 G A ---	---	GATCAACTGTATTGCCAGGCCAGCTCCTGAAGAAGTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGCCCAAGGATTATT
J04162	134 T C ---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTGAACTTTCTCTGGATTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTTATCCAACCTCTCGA TTCJTTCCTTGGTCTCCAGTGAAGGGGAAAGCCCATGATCTCAAGCAGGGAAGCCCCCAGTGAGT AGCTG
K01506	63 T C ---	---	CTGAACCTCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTCTCACTTTCATGTGAAAACCTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCAATTCCT TAGTAAAGTTTCCAACAATAAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTTC ATTGAGCCCTTTATCCT
L18877	69 T C ---	---	TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGCC CT/C]ATCCATTAGTTCCACTGCCCTCGTGTGACATGAGGCCCATCTTCACCTCTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTCTTATTGGATGACTTTGAGATTTATCTTTGTTTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	GCTATTTACATATCCCAAGCCCTTAGGGCTACAG[T/C]CTCTTGTCTGACCCTGTAGGGTGCCA TTTGGAGTTCACAGCCTAGAAGAAGAAAGGCTTTGGCCCTGGTGTGGTGCATAGGCCCTGTAATCGT AGCGCTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAAACCTGGGCAAT GT
L38517	137 G C ---	---	GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATGAGACTTGACTGGCAACACACCGCTCCOCCAC CC[G/C]CGTGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTGACCCCTCT CTCTAGAGACCTTGAG
L39059	123 T G ---	---	ACTTGAGAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGGCAACAATAATACAGTAGTCTTTCTTTGTATTTTGTATATTT/G]CGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGGTGGCCCTGTGTGCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 G A ---	---	CAAAGTTGTCTCTGCCATGAGCACACACAGTCAGGCCCTTGAAGGGATCTTCTAGGGGAGACAACAGC CCTGTCTCAAAACTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGGCCGTGAGTCTGCAT CTTAGGGCATCGCTCTCTCTCACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTCTTACAAATGTCT AAGGT

L48728b	111 T C ---	---	---	AAGTGAACAGAAAGCAAGATGGATTGTTCTCTATATAAAGCACATAGTATGTTTACTGGTATCGT AAGAAAGCTGGAAAGAGAGCTCAAGTTTTTGGTTTACTTTTCTCAGAAATG/CJGAAGAACTTATTTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	---	GGCACAGTCCAAAATACAAATGGACAGAAGATCTATATTGTACCAAGAACTG/AJTATTATTCACC CCATCAAGTATAAGGTTACTGATTGATGGTCTTTTATAAACATTTGGTATATTCCATTCATGCGCAA AGCAAAAGAAAGTAAAGCTAA
M19169	113 T C ---	---	---	TAGGATCTGTCCAGGCCATTGGCACAGCCACACCCACTCCACCCCTGTAGTGTCTCCACCC TGGACTGGTGGCCCCCACCCTGCGGGAGGCCCTCCCATGTGCCTG/CJGCAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTGTTGCTCAGCAGGGGCTCCGCCCTCCCTCTCGCTTCTAATA GC
M21539	114 T G ---	---	---	TCACCTGTTCCACAGCTCCACCTGCATCTTCTCATCAAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCTTAGCCTGTGATCTGCCCATGATATCCCGACAGCAAAATG/GJTTTCTTTCTGAGGCTG CCATGTCGCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCCCTTCAGAGCT TCCTTTGGGTGC
M26041c	173 A G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCTTTGAATTAATTCCTGACTTC CTGATTTTCTTTTCTCA/GJGTGTTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCTTTGAATTAATTCCTGACTTC CTGATTTTCTTTTCTCA/GJGTGTTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCTTTGAATTAATTCCTGACTTC TTCCTGATTTTCTTTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 G C ---	---	---	TAAGGACGCTGCAGGGAGGCCAGTCACAGTCCAGCAATTCACAACCCACTTGAC/GCJAATGCT TGCCAAAGCTGTTTAAAGCCCAAGAACACCCCTTCTTTGTTCCAAATTAACCTTAGAAGAAACCCCA CAATTAAGCAATTCATC
M81695	34 G A ---	---	---	ACTTACTTACCCTCACCTGTGAGGCTGACGGGA/GA/GAACCACTGCACCACCGAGAGAGGCTGGG ATGGGCTGCTTCTGCTTTGGGAGAAACGCTTGTCTGGGAGGGGCTTGTCTGTCAAGGTT CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCCCAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166	C T ---	---	CTCCTCCTTTATTTGAGCATGGAGGGTTTAAATGGAGGATCTCCTTTCTGTGACAAAACATCTTTC ACAACTACCTTGTTAAGACAATTTAAAAAGATCTTTTACAACTTACCTTTGTTAAGACAAAAT TATTTCCAGGCTATTTAATACGTACTTAC[C/]JGGAAATATTCTATGTCAATGATTTTAAAGCTA TGAAATACAAATGGGGGA
U09607	39	T C ---	---	GAGGCTTATGAGGTCTCTACTTCAGGAACACCCCAT/C/GACATTCGATTTGGGGGGCTCCCG TGGCCTGTAGAATAGCCTGTGGCCTTTGCAATTTGTTAAGTTCAAGACAGATGGCATATGTCTAG TGGGGCTCTCTGAGTCTCTGGCCCAAGAACCAAAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	T C ---	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAAGCGTTGATTCCAAAGGCCTCATCTGGAGCCTC GGGAAAGTCTGGTCT/CJACATCTGCCCGCCCTTCCAGCCCTTCCCAGCCCTCCTCTTGTTCCTTC ATTCATTCAACAAAATTTGGC
U10694	20	C G ---	---	GTGACATGAGGCCCATCTT/C/GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTGCTGCTTCTTGTCTATTTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAAATGTTCTTTAATGGTCAGTTTAAATGAACCTTACCATCGAAGTTAA TGAATGACAGTA
U13877b	162	T C ---	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGCACAAGTTGTTTAAAC CTCTTTGTTTCAAGAAATTTCTCCATGGAGTAACAATATCTAGGTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGGAACAGCCAGAGAT[C/]JTTACCGTGGTCTTACTAAAGTACATATCCTAACCTTGG GGTTTACCTTCAGCA
U15555	187	T C ---	---	TTTCTGCCACTTTCACCTGGTTTAAATAGCCAGCCAGTCAATAATAGTAGGGAATCAGTCAAGCAA AAATGCTTTGGAAATTAATAAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTCTAAGCAGTCTGGTCCATG[C/]JTTGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122	T C ---	---	TCCAATTTATGGTCCCCAAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTAAAGAACGTCCTTGACAGCTGAGCGATGACACACACAT[C/]JTTGTTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCTCTGGGAAAACAACCTGTCTCTTGG AATTA
U18543	58	T C ---	---	GCACATGCAGAATAGACTCAGCCTATGTCTGATTCAGCTGGGTAGTTCTAGAACCTT[C/]JAGAAG CTCCATCTTTTAAATGTTTTTATTTGTTATGTCCTCCCTCCCGGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAAATAGGACACAGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACTTCC AAGCCTTAGTAGAGAGGCC

U25975b	164 C A ---	---	---	<p>TCACTGCTGTGGCCTCATACCTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT  ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAAAATGACTATTCTCTG  AAGACAACCAAGAGAAAAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG  GTCCAGAAGGAATTGTGGACTGA</p>
U25975a	143 C G ---	---	---	<p>TCACTGCTGTGGCCTCATACCTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAAATTATT  ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAAAATGACTATTCTCTG  AAGACAAC[C/G]AAGAGAAAAATTGCAAAAAGAAGTATGACTTTTATATGAACCCCTTCTTTAGG  GTCCAGAAGGAATTGTGGACTGA</p>
U25997	61 A G ---	---	---	<p>CAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCA[A/G]TT  TTGAGTGTACTGTGCCTGGTTGATTTTAAAGTAGTCTCTATTTCTATCCCTTTAAAGAAAATT  GCATGAACTAGGCTTCTGTAATCAATATCCCAACATTCGCAATGGCAGCATTCGCCAACCAAAA  TCC</p>
U28413	29 C T ---	---	---	<p>ATTCCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCTCATGTTTAAATGAGGTT  AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTAGTCAAAATGTCTCTTGATCC  CAGATGTTGTGGCCTGGGAAGCCCTCATTTGCTACAGTACAAAGTAAACACAGTCGTTGACCTCAGTT  G</p>
U30884c	89 A G ---	---	---	<p>TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT  CTTCTATCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGATCATAAGACACAAATCTAT  TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTGCCACACAGTTGAACACAAAGT  GCTGTCA</p>
U30884a	34 A G ---	---	---	<p>TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGC[A/G]GTGATGATTTTGGGACCTGCCGTATAATCT  GTTCTTCTATCCACGTTAGCCAATTTGTTCTTGATGAATCTATATGATCATAAGACACAAATCTAT  TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTGCCACACAGTTGAACACAAAGT  GCTGTCA</p>
U31216b	78 A G ---	---	---	<p>GGGACAGCATATGTGGCACCCGCTCTCTGTGCAAGTGAAGACCAATGAGACGGCCTGCAACCAACA  GCCGTATCA[A/G]CCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA  CCAGCACCAAGACCCCTTACAACGTAGAGGAGGAGGATGCCAGCCGATTGCGCTTAGCCCGCC  TGGTAGCCCTTCCAT</p>
U31216a	70 G A ---	---	---	<p>GGGACAGCATATGTGGCACCCGCTCTCTGTGCAAGTGAAGACCAATGAGACGGCCTGCAACCAACA  GCC[G/A]TCATCAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA  CCAGCACCAAGACCCCTTACAACGTAGAGGAGGAGGATGCCAGCCGATTGCGCTTAGCCCGCC  TGGTAGCCCTTCCAT</p>

U31416c	76 G A ---				AGTTGCCAGTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G]CCACAAATCTGGTGCCCTCTCTCTGCTTACAATGTCTAGGTCCCACTGCGCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACCTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ---				AGTTGCCAGTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C]TTCTCAGCGCACAAATCTGGTGCCCTCTCTCTGCTTACAATGTCTAGGTCCCACTGCGCTGCTG GAAAGAAACACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACCTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ---				ACGGGTACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTTGTTCTCC AGCCGCGAGG[C]TTCCCCAGCCTCAGTTGCTGGAGCTGCACATGACTGCATCCTGCTGCCAGG GCTCAAAGCAAGGCTTCTCTATCTGGGGACGCTGCTGAGAGAGGCCGAGAGGCCGCGCAGAAC ATGCCAGGTGTCC
U37690	54 A G ---				GACCACGCTGAAACCCACCCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT[G]CCCCGAAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCTGGCCGCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C ---				TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAA[C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATAACCACCGCATGATTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T ---				TCAAGAAGGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGGTAA AACCACCTGAGCCTCTCTGAGACCATGTGGTTTTAA[A]TATCCATAAGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAATTTGGATTCTCTGTTTTTTCATGCTCTCCTT GTAACCCCTGAGATCATCAG
X52011b	148 C T ---				AGGAAGATCCCAACCGACCCCTTCTGGCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAGGAGACACATTACAAAGAAAGTTGCGAAATTCGG AAATCTGTTGTGCA[C]TGTCTCAAATGAAACGCCCTTTTCGGCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118 A C ---				AGGAAGATCCCAACCGACCCCTTCTGGCCTAATCCTTTAGATTAGGTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAGGAGACACATTACAAAGAA[A]C]GTTTGGGAAAT GCGAAATCTGTTGTGACGCTCAAATGAAACGCCCTTTTCGGCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGTCTCTCCACAG/GTGCACAGCTTCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAATCCCGAGGCCCTCCAGGACTGGGCTTGCCAGGCTTGCCAAATAGCAAGGCCAG GGCAGCTGGAGACGATCTTGTGGCAGGGCCTGGCCTTGCCCCAGGCCCACTGGCCCCCTTCTCC
			AGCAAGCAGTGC
X54869	99 A G ---	---	AAGCATTTGCGTTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATGCAT AAATCTGAAATGAAATATGTTATTTGCTCT/GJATACAAAAATTTAAATCAATATTGAAATAG GATGCACACAATTAATAAGTACAGACATCTAGCATTTGTGGGCTCATTTTGTCAACATGGTA
X66924	147 G A ---	---	GCGGTCTCTGACACCTCCAGAACGCGAGGTGCTGGGCGCGTTCTGCTGGGACCCCGGGAACCTCTC CTGCGGAAGCGGACGGCAGGATGGGCCCCAACTTGGCCTGCCACTTGACCTTCAACAAATCCCT TCCTGGAGACT/GAJAACCTGGTCTCAGGAGCGGAAGGACTGTGAACCTTGTGGCCTGAAGAGCCAGA
			GAAATGTGAAGAAATGTGACAAAAGCCTTTAAGCGGTGTGCACACTTGATTGTATATAAGATAA/T/GJT CATACTGGAGAAAACTCCAGAAAGTGTGACAAATGTGACAAAACATTTAAATTTCTCATACCTTA TTGCACAGGAAAGCATTTATCTTGAGAAAAATTTGTATAAAGAAATGGAAGTCAATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X78932	62 T G ---	---	CTCAACCCATAACCTCAACCACATCT/CJTATCCTCCACCCACATCCACACATCCACCTCCATCC CCAACCCATCCTCATCCCCAATACAGCCCCAAACCCAGCCCCAGACTAAATCCACAGCCATCCCCAA CTCATCCTCATCCCCAATGCAGCCCCAAACCCAAACCCAGGGCCATCCCCAAACCCATCCCCAAGCC AACTCAACACCATCC
X80026	25 T C ---	---	ACCCAACTCAAGTCCAGGCCCGAGGCATCTTCTGCCCCCTGCTTGGCCCCATCCAGTCCAGG CGCCTGGAGCAAGTGTCTAGCTACTTCTCTCTG/CJACATTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAGGCCACCCCTAGAAAG
X80197b	99 G C ---	---	ACCCCAACTCAAGTCCAGGCCCGAGGC/GAJTCTTCTGCCCCCTGCTTGGCCCCATCCAGTCC AGGCGCCTGGAGCAAGTGTCTAGCTACTTCTCTGCACTTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAGGCCACCCCTAGAAAG
X80197a	28 A G ---	---	GGCACCCAGAGTGACCAAGTCCAGAGGGAGGGCGCGCGCTGCGGTGTCGGTGTTCCTTTT CAGCCCCGAGAGGTCTGACCTGGGGCTTCTCCAAAGCTACTGCGCCAGCTGCCCGCCGCTCT CTTTTCTCCCAAGC/GAJAAACCAATGGGCCCCCTTCACTCGCGTGGCGGCGCGGGGGCTT CTTTCAGAGC
X85106	150 G A ---	---	ACCACAGCCATGGTCTAAGGACATGGATCGGGTGCCCGGAGCGTGTGCACAGGGGACCCCTCTGCC CACTCTGGGCTTTTCAGATCTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTT/GJGGG ATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACCTGTCCAGGCTGAGATAAATCCC GGGA
X87160	128 T G ---	---	

X87344	34 C T ---	---	CATCCAAAGGCACTGGTGTGACTCTGCTTCTGTC/TTACTGACCCAGAGCCTCTGCCTGTGCACTGC AAGCTGTGTCTACTAGGCCCCAAGGGGACTCTCTGTTCCATTCTCCCCACAGACTGTCAAGAG AAGCATGACAAACAAATCATTTACCGACTTTAGTGTCTTTT
X87838	179 G T ---	---	GGTGGGCTGGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCTATGGGAACAATTGA AGTAAACTTTTGTCTGTGTCCTTTTGGTCGAGGAGTAACAATACAAATGGATTTTGGAGTGACTC AAGAAGTGAAGAAATGCACAAGAATGGATCACAAAGATGGAATTTA/GTTCAAACCCCTAGCCTTGCTT GTTAAAAATT
Z14138	81 A G ---	---	GTTCTGCTGCTCTACACAGGGGCCCTGTACAGTGAATGGTGCCATTTTCGAAGGAGCAGCAGTGTGA CCTCTGTGACCC/AGTTGAATGTGCTCCCAAGCGGCCCTGTGTGTTGACATGTGAAGCTATTTGAT ATGCACCAGGCTCAAGGTTCTCATTTCTCAGGTGACGTGATTCTAAGGCAGGATTTGAGAGTTTCACA GAAGGAT
Z18859	191 A C ---	---	TAATCCTCACCAATTCCTCAGGTATAAGTTCTATAACAGGCTTGGAACTCTGGGTAATTTAAACACAGA AAATTATAGTCAATATACCATGACATGAAGAATGAATCCATTCTTTGGAGATGGAGTATACATGACT GCAACTGTATTTTCATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGC/A/C/CAGGTTTC CAGTACTGGTTTTCCAA
Z23091	159 G A ---	---	AGAACTGAOCAGATGTGGCTGGAGGGGAATCCAGACCCGCTGCTGTCTCTCCCTCCCTCCCTCC CACTCCTCCTCTCTCTCTCTCTCTCACTGCCACGCCCTCTCTTCCCTCCTCCTCCCTCCCTCCG CTCTGTGCTCTTCAATTCAC/AGGGCCCGCAACCCCTCCTCTCTCTGTCCCGCCGCTCTCTGGAAA CTGAGCTTGACGTTTG
11595b	125 A G ---	---	GTTGGCATTGTTAGTAAACTTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAACCTGACCCCTAGTTGTCTCCAGGACCTA/AGJGCGTGC TCACTCTACCTTGTCTTTGTGTTGAAGAGGTGGTTCCCATGACTGTTTAAAGTGAAGTGCCATGG ATATCTACACCGTCACAGACTAGATTGTCTCAATGTCTTGGCTTGGCAG
11595	125 A G ---	---	GTTGGCATTGTTAGTAAACTTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGGTTTCTGCAAGGGCAGGTTTGAACCTGACCCCTAGTTGTCTCCAGGACCTA/AGJGCGTGC TCACTCTACCTTGTCTTTGTGTTGAAGAGGTGGTTCCCATGACTGTTTAAAGTGAAGTGCCATGG ATATCTACACCGTCACAGACTAGATTGTCTCAATGTCTTGGCTTGGCAG
1241	131 G T ---	---	TATATCACATTAGTATGTCACTGCCATGGTAAGGACTTTTGATCACTAGGAAATAAGAACACTTTTGAA TGGTCTTGTCCCTTTCAAATAAAAGAGTGACATGATTGAACATGTGTTTATAGATAAAGGGCAGCTT/GT JGCAGGAGTGTTTAGGATGAAGAGAGAGAGAGATTAAGGAAGATCAGGAAGAAAAGTAGCAATGGGA ATGAAAATAGGAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAAAAG



1282	130 C T ---	---	GTGCGATCACCACACTAGTCTAATTTACAGATGTTTTTCATTACCCCTAAAGAAATCTTTGTACCCCATTA GCAATTTATCTCTCATTCCTGCCCTCACCCCGAGCCCTACTCTTTATCGCTATAGATTTGCC[C/TTACT TGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACTGAGAATA ATGTTTTCAAGGT
6810	68 C T ---	---	AGTATCACACATACTTAAATATATTAGATATACACAATAATAAAATCACTCCCTACCTTGAAAACCTTT A/C/TTJAGAAGCATTTTTAAATTTTACAACACAAAGCTCAACGAACCTACAAATAGTCTAGTAGTCTG TTTACGTGCCAAGGGATAAGGCTGAACATAAATTAACCCCTTTAAAATGTCTATGAACAAGTACAA TTTTCTTTTGGAGTTCTGCAGAGCAATGACCCTAAGAAATATTTTTAAAGGC
6817	118 A C ---	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTGCTTTTGTAAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC[A/C]TGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGATCATCAAAAGATGTTGGACACCTTGTGTTCAAATC TTGGTTCAAGTGGCGCCTGTCAGATCGGCTTTTGGTTGGTGTCTAG
6819b	212 C ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAGACTTTTAAATGGAACAATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166 G T ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAGACTTTTAAATGGAACAATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39 A G ---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATTGTTTACTATGGCACCAATTTGGGACA CAGATTATATATGTCAGACACCAACGAATGTCCTTTAAGATATGCAGCAAGCACAATCTGTCTATGGT TTAACAAGAAATGAACGCTTAGG
6972b	149 G T ---	---	AGGATTCCTCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCCTTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGACTCTTTTGGTTGGTAAACTATTGATTATGCG CACAATTCAGAG[G/TCCTGTTATTGGTCTATTACAGAGATTCAACTCTTCCTGGTTTAGTCTTGGGA GAGTGTATGTGTCAGGAAT
6972a	122 A G ---	---	AGGATTCCTCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCCTTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGACTCTTTTGGTTGGTAA[G/CTATTGATTA TTGCCACAATTTACAGAGCCTGTTATTGGTCTATTACAGAGATTCAACTCTTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCAGGAAT

7598k	210 A C ---			AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTTATTTCTTGAGGATGCCCTTTTA ATATTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208 A T ---			AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTTATTTCTTGAGGATGCCCTTTTA ATATTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGC[A/T]GA
7598i	192 G T ---			AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTTATTTCTTGAGGATGCCCTTTTA ATATTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTTATTTCTTGAGGATGCCCTTTTA ATATTGATCC[C/T]ATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTTATTTCTTGAGGATGCCCTTTTA TTAATATTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTTATTTCTTGAGGATGCCCTTT TTAATATTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTTATTTCTTGAGGATGCCCTTT TTAATATTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCC[C/T]GCTAACCCAGATTTTACCTTGGAGAAATGAAAATTTATTTCTTGAGGATGCCCTTT TTAATATTGATCCCAATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACAC[C/G]CCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAAATT[A/G]TGATTTACAAAAGACACCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTTCCCTGATATGTTATCTTTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACCTTTAATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATA[A/T]CCTTGAGGTTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACCTTTAATGAATGGGTAGTCT[A/C]TCTCAAGGTCCCAATAACCTTGAGGTTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACCTTT[A/T]ATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAACCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAATGGGTCCCAATAAAATGGAATTTTAGGGCAACAAAAGTCTAAAAGGCC[A/G]CAAAAAGAGA AATAGCACCACGTGCAATTTGAACAATGGCTAGTTACTTTGGCATTTTGGCATTTGTTAATCACTGAATC TGGGTTTTCTCTGAATTCACACAGAGCATGCACTACACAACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACCTT TGACGCAAAATCCACTTTGCTGTAA[C/T]GGTCATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGTCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACTG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACCTT TG[A/G]CGCAAAATCCACTTTGCTGTAAAGGTATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGTCATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACTG
8498	84 C T ---	---	AGGGTTTCAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACCTTCAATTAATCGAAAAAGAAAAATTTGCTTTAAGGAAAAAA AATCCAGTTTTAAGAACAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCCAGGAATGTAATTTTCTTAACCTCAG

WI-18562	29	G A	---			CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C	---			ATAGCAGACTTTTAATCAATGCCAGAGACAAAGTGAGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGTATAATTGTAACCCACAGTGCTCGCACAGTTG AC
WI-18683	22	C T	---			TAAGCTGTTTCAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAATAAATTTCTCTCCCAAAGCCTGCCTGCAGT
WI-18520	75	G A	---			GACTTTGGTGATTAAATGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACCTACTGCCAACAAACACGGGCATCCACTCTGTCTTCAA TGCTCTCCGTGAGAC
WI-18563	94	A G	---			AAATAAGTTTATTGGCACACAGCCAAAGCCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T A	---			GTCTATTTCAAATTTAGCTAGACCCATTTCATCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G A	---			AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAAA[G/A]TATAAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T C	---			AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAACCAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96	A G	---			TTTATTACAATAATTTAGGTGGCACAATACTAACAAAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCA TAGACTTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18619	44	G A	---			TTATTCACAAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGGAGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGAAGGGTATTTTTTAATAAAAAATAA TGGAGCTACAACCCACCC
WI-18715	76	G A	---			GTAAATAAGTTTTATTGGCACAGCCAGCTCGTTTCATTTCATATGCAATGACATCTGCTGTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGTGGTCCCGTG
WI-18535	107	G A	---			AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCATTACTAGTTTTTTCAGTTCTGGCAGGTGAC TTTCATCTCTCGAAGTTCAGTTTCTTCATAAGATGGAAG[A/C]TGTCTACCTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGATAGTACACTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAGGTGATGTCTACAGGACGACGAAG
D17525	107	C T	---			

DWU-133c	313	A G ---	---	TAATTGGCCACTGGCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAAGATTGAGATCATGAATGACTGACAGAAATATTTGTTGGCAGTCCT GATTTAAACCTAAGACTGGCTTGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCACTGGCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAAGATTGAGATCATGAATGACTGACAGAAATATTTGTTGGCAGTCCT GATTTAAACCTAAGACTGGCTTGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCACTGGCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAAGATTGAGATCATGAATGACTGACAGAAATATTTGTTGGCAGTCCT GATTTAAACCTAAGACTGGCTTGTTAAATGAATATGTCAGTTTGAATTTAATAGTAACCTCC ITCCAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAACGTTTGTGTGGTGGCACCTCTACGTCACAAATGAAGTG TGTTCCCTCAGTGCATCTGGGAAGATTCTACC[C]TGACCAACAGTTCTCAGCTTCCATTTCGCC CCTCATTTATCCCTCAACCCAGCCAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAGGATTATGTTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAATGCAACTGTTGATTTCTCAACATGGCTCACAAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTTAGTTTAAACTGCACCTGCCAACAAAGTTCACTTCATATATAAAGCATTATTTTA CTCTTTGAGGTGAATATAATTTATTAACAATG[G]TAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTACCAGATATCAAGTAAATACACAAATGAAGTGTCAATTATCAA
DWU-447b	172	--- ---	---	ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAAGCTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATTAGTTTGATTAGAGCACAAGCTTAGCTAATCAA CCATTATTTTCAATTTGTTTGTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTGTTAG GCCTTCTTTCTTACAATGAAGAGATGATTCTCTAGTTTATGGTTA
DWU-447	85	A G ---	---	ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAAGCTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAA/GJATCACTGTAATTAATTAGTTTGATTAGAGCACAAGCTTAGCTAAT CAACCATATTTTCAATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGCTTTCTG TTAGGCTTCTTTCTTACAATGAAGAGATGATTCTCTAGTTTATGGTTA
DWU-476	63	C G ---	---	GTAAAAATTCAGTTTCTCCAGTTCCTCTTTTGTGCTGCTTCTCAATAGCGTTTAAAGGTGAG[C]GJAT AAATCAACTGTCCATCAGGTGAGGTGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T ---	---	---	TCATAAGGGCAGTATCTCTCTAGCTAGTGGCCCATACAGAAAATTCTATCACCATACAAAATTTA[ A/T]TGCAGTATTTATGTTTTAAAGCACAGGTGTACCGAAACTGTGAAAAGTCTGAATTTATGGGTT CTATGCATGCAATTTTGCCTAACCTAGAGAAAGAGTTTGATAAAATTTTACCAGCTTTGAAGATGGAT TAACTTTTGACTTTGAGCTTTAAACTTTTAA
DWU-512	131 A G ---	---	---	AAATCCAGGCATTTTGAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAAGTCCACTTATTTAA AGAGCTTCCACAGTGAAGATGGAGAAGGTGAACCTGCTTTGAATATCCAGATGTGTTTGGTC[A/G] TGCGTATGGCAGTGAGCAGGTATGTGTTTGTCTTGTCTGCACTGAAAATTTAAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATTCAGATGTCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	---	AACTGCATATAGATAAATTATCCAGGATGTGGCTCAATCTTTTCAGCTTGTCTTCTACTACTGTTTGTGA ATATACAGTTTTTGTAAACCATATGATTGA[A/C]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATCTTGTCTTTTCAAAATATAGTTGAACAAGATTTCCCTTAAAAATT CCACCAGGATTAATCTCTAAAAATCTAGTCTCTGATTTGC
DWU-59	94 C T ---	---	---	CATTTCTTTGTAAAGGTAATGGACTCACAAAGGGGAAGAAACATGCTGAGAATGGAAGTCTACCGG CCCTTCTTTGTGAACGTCACTTGGC[C/T]GAGCCGTGTTCCAGGTGGCAGACTCGTTTTTG GTAGTTGTTTTAACTTCCAAGGTGTTTTACTTCTGATAGCCGTGATTTCCCTCTCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C ---	---	---	CTTGATCATGGGTGGAAATTTTGTGATCTGGGCTTCATGGGATGCATAAAAATTTCCAGTTGGTAAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	---	CACACTGGCATCTAGGCCCTTGGCTGCAATTCAGAAAGGAGAGCCAGTCCCCCTCTCGAGAA[C/T]G CTGGTTCCCCAGCCCCACACCGGCTTGCACACACAGGCTGTTGAGGCGAGGAGGTGGTAAAGACGT AGCTGTAGACCCAAAGCAACCAAGCCCTGGGACCCCTCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCAATCCCATCATTAGACAAGACACATCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAAGTGCAACCATCAGAGT GTAATTAGGCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A ---	---	---	TTCCAATGTAAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTAATCTTTTCATAA[T/A]CTGACAGGTCAAGTAAGTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	---	TTCCAATGTAAAGAGTCAAGTACCAAGTT[C/A]AACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTAATCTTTTCATAATCTGACAGGTCAAGTAAGTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	---	TGTAAGGTGACTTCTATAAGCTTCTAAACTGTCAAACCTTCAATTTACTGAGATTATTTACGGCCAAAT GTGTC[T]TGTGGGTCTGAGATTGATTATCAGCTGGGTAAGTTAACCTGTCTCTGTTTCA

WI-18063	105	G A ---	---	AGGCTTTAAACTGATAACAAATTTGCCCTTTAATCACAATACAAAACCTGACACTTTCATTCCTTCCTTC CCATGTTTCTGATTTTGATGTAACCTTAAATTTGTTG[A]TCTTTAACAATATACTGTAGCTGCA
WI-18078	86	A T ---	---	AGTTGAAGATCAGAGAGGTTATGGTTGGTAGTACCTGAACTCAGATTCAAACCTGGTCCAGTGTG TTGTTTTTTCAGCATCAG[A]TGTCCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C ---	---	CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTTTCATCCTTTGTTAATTCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGACTT[C]GGGGCTTTTTTATACCTCCATATCTCAACTTGTAAAGC
WI-18119	38	T C ---	---	GCAATCTGTAACAGTTTGGTAGTGTATTACAGAGGAT[C]TTGTAAATGGATTGGAGTACTTAC CACTATTTTCATCTGCTCTGAATAGTTCACTAACCAACTACTGACAACAGTTTAATTTTGGTTCTT
WI-18142	66	T G ---	---	TTCAAGATAATTACAAATTGGAAGGGGACCAATAATTCACATTTTAAATCGAAAAATACTATATAC T[G]CCCAATAAATCAGTAAATAAGCTTCAAAAAGCCTTAAAGACACCAAAAAGGAAAA
WI-18178	68	T C ---	---	GCATAGGGTTGAGGGGTGTACAAGAGGAGAACCCAGATTCACTGCCATGCCCTGGAGGTTAGTCTGGGG GT[C]CGGGCGGATGGACACACAGACAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	G T ---	---	TCATCTGAAAACCTTGTGTAGCCAGCATGGGGT[G]TGGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACCCAGTGCAGGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A ---	---	ACAGATGTCAAGTTGTTTGAATTTGGCCCATTAAGTATGGGGCTTTCTGTTAAAAAGTCATCCAA AGGCTTGGCAAGAGTTTGCTATACAAAGGAGGACAGAGAAACATGA[G/A]CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18261	26	G A ---	---	GATTTGAAGGGGATTTGCTTTATTTAACTG[A]TGAAAAGCGTGATAGAGGAACCTGTTAAGATAACAA CTTATAAATCTCCCAATTTGTAGAAGTGAAAGATTG
WI-18268	88	C T ---	---	TAGGAGGGAAGAGGAGGTGGGCTGCCCTGGGCCCTCAAGACATGAGAACGGGTGGTGGCTTCCAAGC TTCTTACTTCCCCCATAGAT[C]TCTGACAATGTGCTGCAGAGCCCTCCAACTGGAAC
WI-18299f	107	C A ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAATTTTGA[G/A]GAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299g	101	A G ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTGCCAAATTTTTT ATCTATTTG[A]GTCTGAGAAATCCACAATTTTGAAGAATTTCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299d	77	G A ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTGCCAAATTTTTT T/GJATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAATTTCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299c	67	T G ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTGCCAAATTTTTT T/GJATCTATTTGGGTCTGAGAAATCCACAATTTTGAAGAATTTCTTTTGCCAAATTTATGACATATCTG CAG

WI-18299b	52	G A ---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAGATCATTAACCTTG[G/A]TTTGCCAAATTTT TTATCTATTGGGTCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299a	48	C T ---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAGATCATTAACCTTG[G/A]TTTGCCAAATTT TTATCTATTGGGTCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18307	76	G A ---			TCAACTGTACCAAGTTTAGCAGCAAGAGGATACTTCTTAGAGACTTTTCAAGTGGACTTAAACTCAG TTCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC TTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACITTAACCTCCGGGGGGTGGGTACTGATT TATC[C/T]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18324	72	C T ---			ATGAAAGTCACCTCAATCATAGGTCAGAGAAAGAATGTTTCAGAT[C/C]TAATCTATGAAAA GGTGTATCTGCTTGCAATTTAAGAAACAACACAAAGTCA
WI-18350	48	T C ---			TCCTGACATGATCTGTGAAATAACGTGATTGTGGTTGAAATTCCTGGAAAAATTTGAAGATAAAATTG ATTATTCAG[G/C]TGTCATTGGTTTATACATATCTCTCTCTTAATGCAAGCTATG
WI-18395	77	G C ---			TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG GATAACATTGCCAGTATAACCAATAATTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18398	62	G T ---			CTCGTTGGTATTCTCTCATCC[C/A]TTCCTTTTCGCTCTTTCTAAATTAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAAGTATCAACTTGTACAAAAGTC AATGAAAA
WI-18396	21	C A ---			AAGATGGGAAAGAGGAAATC[C/A]TTTTCTTACTAGAGATTTTTTCCCTTTAATCCCTTTTCAAT TCAAGGATCATCAAGGAGCAGGTGCAGAGCTCTGGGGCCAGAGGCCCAAGTGCTA
WI-18409a	20	C A ---			AAAAAGGAAAAAGGATGGAGTAAGAGAGAGACAGAGGAAACAAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGGAAACACAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18442	62	C T ---			TTGATGTTAATACTGTCATTCTGGAGATCGGCTAAAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTCGACAGATTTAAACAAGTAAGACATATATCAACCCCTCATATTTTCCAAACA
WI-18452	38	G A ---			ATATAAGCTGGAGACTGTGGAGGTGAGAGGAGTGGGACTAGCTGTTGAAAGAGAGATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
WI-18489	102	A C ---			CTGGTGGGAGGAAACAAATTTGGGTATATTATACAAATGGAAAACTCTTCAGAAATAAGAAAGGAA CAACCACTGAATCACACAACATGGACAAATCTCAATCATTTATGCTGATGGAAAGAAACCAATTCA TAAGAATACACAGTACAT
EST5b	93	A ---			



EST5	93 A	---	---	---	CTGGTGGGAGGAAACAAATTGGGTATATTTCATACAAATGGAAGAACTCTTCAGAAATAGAAAGGAA CAAACCACTGAATCACACAACATGGACAATCTCAAATCATTATGCTGATGGAAAGAAACCAATTCAT TAAGAAATACACAGTACAT
EST6	48 C	---	---	---	TTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCAATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAGCTTTTCTTTCTTTTGCACAAAGACAAAGCAAGCCACATTTTGCATTAGACAGAT
EST8	158 A	---	---	---	GGACAGGACCTTATTCGCCCTGTGAGCAGCGGCTGATGGACTGAGGCCCGGAGGATAGTGGGCG CTCTCTCAGGGGCTCTCAGGACCCAGAGCTGTCTCTGTTGAGTTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCTGAGTTGCAAGCAGATGGAGATTGGACACTGTGTCTTTGGTGGGT
WI- 18740c	104 G	T	---	---	TCCTCAATTGTTGGGATGATGAGAAGAAATGATTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCATTTACCATCATGTATCCAGTAGTG[ <i>G</i> ]/ <i>J</i> ATAATTCAATTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C	G	---	---	TCCTCAATTGTTGGGATGATGAGAAGAAATGATTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCATTTACCATCATGTATC[ <i>C</i> ]/ <i>G</i> JAGTAGTGGAATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 C	T	---	---	CCAAAGTCTCTGTTGCTCATAAAGAGTTTGGGATGGGAGAGATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCTTCTTTACAGAGGTAGCACAA[ <i>C</i> ]/ <i>J</i> TGATTCCAACACAAAACCCCTTCCCC TTTTAAATGATTCTGTTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTTTCCCTCT TGAAGCAATGACAAGCACCTTACTTCACGGTGGTTTGTCTTTCTAT
WI-18746	114 G	A	---	---	GCCAGCAGCTGAAGTCTCTTTCTCTCTCTGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGTTGACTTGACCGTTTTTATATTACTTTTGTAAATATCTT[ <i>G</i> ]/ <i>A</i> JTCCACATTTCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112i	212 G	A	---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCCCTGGTTACGGCCCGGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATCAGTAGTGCTATCTCATGACAACCAAGAAACCCGACGACAAA TCCTTTGCGAGATTTCTCTAGTGGCTTAGAAACATGGCTTTAAGAAACACACGGTATATCTTTGAG GGTGACAAGGC[ <i>G</i> ]/ <i>A</i> JTCTCTTCAACAGTTCATACCAACTGCTTTGCTCTAG
WI-19092	232 A	C	---	---	TGGTGGCTGGCTAGTAGTTTCTACAGAACATAATTTGCCCTATAGAGGCTATTTCTTAGATCATGT CTCAATGGAAACACTCTCTTTCTTAGCCTTACTTGAATCTTGCTATATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGTCTTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTC[ <i>A</i> ]/ <i>C</i> JATGATTAGCCGTGAAC
WI-19057i	175 G	A	---	---	CCCATTTATTAGGCCAGTGATGTCTCAAAGAGTAGAGGAGCGTCTACTGGTCTTTCAACTCCTTCA GTCTTCTGACGGCGGACTTTACGTGACAGCGGAAGTGTATTGTACGTCAGGCAACCGCAGCCACTG TCTTCATGCAAGGAACACAGTGCCAGATCCCCACAGCTC[ <i>G</i> ]/ <i>A</i> JTCTTCTCACTTGTGTTTGGCCACA

WI-20103	168 C T ---			TGGGACTTCCAACTCAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGTCTCCCA/C/JTTCATCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ---			GCCTTACCCATTTGCACATATATACATATGCACCACTTTCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTGTAGGACAAGAAATGGA/G/JTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTTCACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ---			TGGTTACAAACCTAAGCCCATATACAAAATTAGAACACATTTAGATGCCTCTTTTGAAAGAACGT TTTAGTCTTTTAACTGAGTTTAAAAAAAATAACAATGCAATTTTTTA/G/JACACTGTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA/G/JAAAGGGAGTTTCCACGACGCCAGTGGTGAGC TGC
WI-20613b	156 A C ---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA/G/JAGTTGAAAAAAGGGAGTTTCCACGACGCCAGTGGTGAGC TGC
WI-19984	47 A G ---			CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAATA/G/JTATAACATTAGAAAA GCAAAATTTCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAATGAAGGCAGTTTTCCAAATCTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ---			GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCAATCAGGCAATA ATTGTTTCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGGACTTACACATTCAAGTTTGACAGI T/C/JTGAANAACCAACTGGAGCTGCTTTTCCAAAGATGTTCTGTGTCCTTCAAAATAGGAATTCATG TTATTTCTTCTTGGCCTTAAGCTCTTATATCTTTCAAAATGACCTAAGCTGA
WI-18846a	49 G A ---			GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCT/G/JAAAGCTGGGAGCGT GGGCTCAGCAGGCTGTGCTCCATCCCGTAAGACCTCCTTCCCTTCCCTCAGCAGGCCCAACATG GCCAGACTCCTT
WI-18959	123 G A ---			AGCAGTGGCCTTATGTCATCCAAACCCAGCCTCTTGACAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTTACTACAGTCTTTTAAAGTGAATATGGTCGAGAAAGAGGCACCG/G/JGGAAGCCG TCCTGGCCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCAT GTCTGGACACACACAGACTATTTTAGATTTCCTTTGCTTTTGCAACC

WI-20146	31	T C ---			---	TGAGTCTTCTGTAAATTCATTGAGCAGTTAGCT/CJCAATTTGAGATAAAGTCAAAATGCCAAACACTAGCTCTGTATTATCCCCATCACTACTGGTAAAGCCTCATTTGAATGTGTGAATTCATACAGGC
WI-18922	74	G A ---			---	TAGGAATTGGTTTCACGCCCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGACTTAAGC[G/A]TCTGGCTCTAATTCACAGTGTCTTTCTCCTCACTGTATCCAGGTTCCCTCCCAGAGGAGCCACCACTGCTCTC
WI-18763b	53	A G ---			---	TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA/GJ/TATTTAGAATGTACCATAATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGTTGATGAACGTCATGTGTTTTGGCCAA
WI-18763a	38	A G ---			---	TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGA/GJ/TGACGATGATGTGAATATTTAGAATGTACCATAATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGTTGATGAACGTCATGTGTTTTGGCCAA
WI-18771b	75	G A ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACTGCTCTCGGAGGATGCCTAGAGATGTTGGGAACAGAA[G/A]AAATAAACTGAGTTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57	A G ---			---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACTGCTCTCGGAGGATGCCTAG/GJAGATGTTGGGAACAGAGAAATAAACTGAGTTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70	T C ---			---	GGGAAAAATTTGAGACGCAATACCAATACTAGGATTTTGGTGTGGTGTGTGATGAATTTCTGAGGCCT/CJTGATTTAAATCTTTCAATTGATTGATTTCCTTTTAGGTATATTGCGCTAAGTGAACCTTGTCA
WI-18742b	51	C T ---			---	ACAAAGTCCTGTAGCCCCCTCACCTTTCTGTTTTCACITTTTGCCAAATGTAC/JATCGGGTTTGGTTTTCTTGATTTTAAACGGTTGTGGTTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGAGTTTTACC
WI-18882	94	C T ---			---	GTGTGTCCAAAAATGGGGTCTGCTCTGCTACCTTGACCCCTCCCTTCCCTCTGCTTCTCTCCTCATCATCTATTCCCAACAACATCCTCTGCCA[C/T]ACACAACAAAAACGTAAGTTTCATTTGGGCCAAAAATTGA
WI-19970b	167	G A ---			---	TATAAGCCCGAGTACCAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACCCGGCCCCGGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTCTGCCAGTTCTCACTGCGGGGAGCAGCAAAGGCCCTTCTCACTGGTGGTCAAAAG[G/A]TAGTCACCTTGGCCCTGGTGATCCACAGAGGATGTTGTTCAAACCAGAAATCTTTTAAACGACTGACCTTCTTAAAAACAGA
WI-19970a	126	T C ---			---	TATAAGCCCGAGTACCAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACCCGGCCCCGGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTCTGCCAGTTCTCACTGCGGGGAGCAGCAAAGGCCCTTCTCACTGGTGGTCAAAAGGTAAGGTAGTCACCTTGGCCTGGTGATCCACAGAGGATGTTGTTCAAACCAGAAATCTTTTAAACGACTGACCTTCTTAAAAACAGA

WI-19067d	202 T G ---	---	TATTGCTGTGCTACTGCCTGACATTCACGGCAGAGGCTGCTGACGCTCCCTGGCTGTGC ACATTCCTCTCTCTCCACAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCTGAGAAATGTTGTGAGGGTTTATTTTTTAAATAGTGTTCATAAAGAAAT/ GACATAGTATTCCTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGTGCTACTGCCTGACATTCACGGCAGAGGCTGCTGACGCTCCCTGGCTGTGC ACATTCCTCTCTCTCCACAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCTG/CJAGAAATGTTGTGAGGGTTTATTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGTGCTACTGCCTGACATTCACGGCAGAGGCTGCTGACGCTCCCTGGCTGTGC ACATTCCTCTCTCTCCACAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCT/CJGGAGAAATGTTGTGAGGGTTTATTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGTGCTACTGCCTGACATTCACGGCAGAGGCTGCTGACGCTCCCTGGCTGTGC TGCACATTCCTCTCTCTCCACAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGTT CTCTGGGCTCTAGGCTCTGAGAAATGTTGTGAGGGTTTATTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TAAATCCAGCCCTACCTTGTAGTATTTTAGGAGACAGTCTCAAGCACTAAAGTGGCTAATTC AATTTATGGGTATAGTGGCCAAATAGCACATCTCCACGTTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATTTGTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGGCCATAGCCTATAATTGGTTAGAACCTCTCTATTTTAA/TCTGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCACATCTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAACJAGTGTAAATTAATTCACAATATAAAGTTCTACAGTTAAATATGTGCATA TTAAACAATGGCTGGTCAATTTCTTTCTTCCCTTAATAAATTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATGGATGTTTTCATAATACATAAA GTTCTCTGTAATTACAACATAATATTATGCCCTCTTCTCACAGTCAAAAGGAACCTGGGTGGTTGGT TTTTGTGCTTTTTTAGATTTATTGTCCCATGTGGGATGAGTTTTAAATGCCACAAGACATAATTTA AAATAATAAACTTTGGGAAAGGTGTAAIG/JACAGTAGCCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGTAGCCTCAGAAACTGGAATAGCCTTCGAAAAGAAATGTCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTGTGCTGATTTGACCTTGATTTCAAGTTAACTGTTCCC CTTGATTTTGTAAATACCTGTACATACTTTGAGTTCAJ/CJCTTAGTACGTGGCTTGGTCA CTTCGTGGCTGAGGTAGAACGTGCTTGTGGAAGACAACTGTGGCTTG

WI-19042	193 A C ---	---	---	TTTGTCAAGTGTGCCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTTGAACCTTTGTGCTTCAAGGACATTTGGTGAAGTCCACAG ACACAAATTTACTCGACAGAACTTCAGCAATTTGTAATATGTAATAACTCTAACCA[A/C]GGCTG TGTTAGATTGATTAACATATCTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---	---	---	ATTGGCCCTGTACAGTTTGTCTATTATAAATTCATTAAACACTACAGGTGTTGAATGGTTAAAA TGAGGCCCTCCAGTTTCATTTTCAGTTATTTCTGAGTGTGCAGACGCTATTTCCGACTGTATTAAT GTAACCTATTATAATGAAATCAGAAAGCAGTAGACAGATGTTGGTGAATACAAATATTGTGATGCATT TATCTT[A/C]ATAAAATGCTAAATGTCAATTTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ---	---	---	GCTTCAATTGGCGATTGATTCAGTGCCCAACAATGTAACAGGGTTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCTTATTGATTTCT[A/G]TAATATAGGATCCTGGAATGAGACCTGGTGGA
WI-18821b	76 T C ---	---	---	TCACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGTAGCCATTGTGCAGTCATGGCCCGGGGAACTTGCCAACCTTCGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	---	TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A[C/T]AGAGGCTGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAACTTGCCAACCTTCGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	---	ACTCCTCTGCTGTCCAT[C/G]ACTGTCTCTTTGAACCAAGGAAAAGTCAACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAAGTGTCTTCCATCACGTTG CTACCTTACCACACTTCCCTCTGATTTGCGTAGGACGTGGCATCTACTTACGTACGTGGCATAAC ACATCGTGTAGCCCATGTATGCTGGGTAGAGCAAGTAGCCCTCCCTGTGTC
WI-18908	70 G C ---	---	---	TGGAATTCCTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG[C/C]TTAGGGAACATTCATCCTTGAGTCAAAAATCTCAATTTCTCCCTATCTTTGCCACCC TCATGCTGTGACT
WI-19037b	155 A G ---	---	---	CACGGTCTCTGCATCGTTACCAGAGCGCCTTCTGTCTAGCACGCCCTGTATGACCGGCAATA TCCCCAAAGCTTTTGGGTCTCAAGTCATGCCCCGAATTTAGATGCTGGTCATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCAGCTGAGCTGTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGAGGTGG
WI-19037a	47 C A ---	---	---	CACGGTCTCTGCATCGTTACCAGAGCGCCTTCTGTCTAGCCACG[C/A]CCTGTATGACCGCGCAA ATATCCCCAAAGCTTTTGGGTCTCAAGTCATGCCCCGAATTTAGATGCTGGTCATTTCTGGAGAGGG GTCCCTCCCTTACGAACAAAACCCAGCCACATGACTAGCACGCTGAGCTGTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGAGGTGG
WI-19064	66 T C ---	---	---	TTGAGGAGGTGGGTGAAGTCTCTCTTGGCAGGATTTGTGACACTGCATTGCTGGGCTGTGTTCCT[ C/G]GGGCTCTTCTGGACCTTGACCGTGGATACCGGCCATGTGCCATGGTATTGGGTCTCTGGGAGGG TGGTGAATAAAGGC

WI-18972a	112 A G ---			AGGCTGTGGCTTATGTCAOCCACAGAGGGTCTGAGAAGTCTGGCTGGGATGCCCTGGCC CCCTCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGAAGCAG/GTGTCTTGTCTGGCCATGGAGCC TCATTGCAAGTTGTCTTGAACACCTGAGGCCTTCTGTGGCCACCAGGCACTACGGCTTCTCTCTOC AGATGTGCTTTGCCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---			GTTTGCAAAACCAACATGTGCTCTTTTTCAGTCACTTCACTGTTTAAATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTTTAAACGAAGTTCAAAGATTAGAATATACATCTGTGTC CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCACTCAAC/AJCTCAACACTATTGAC TTTTGGGCTGGATAGTTCTGTGTGGGGTTTGTCTTGTGCACTGTAG
WI-19016a	161 C T ---			GTTTGCAAAACCAACATGTGCTCTTTTTCAGTCACTTCACTGTTTAAATGACATGGTAGAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTTTAAACGAAGTTCAAAGATTAGAATATACATCTGTGTC CTGAAACCTTAGATACATAGCCGAC/JTGTATACAGAGGTTCACTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTTCTGTGTGGGGTTTGTCTTGTGCACTGTAG
WI-20096	21 T C ---			GGTTTGGGGCATTTATTTCT/CJGATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---			TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTAACTCCAGCCATG AGTATAAGATTAAAGCAGTTACTTTTATTTGAACAGGAGTGGCATAAGCAACTCAGTGTGCC CTTAGGGTGGGAGCTCTCC/CJCTACCACTCCCAAGGATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---			TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTAACTCCAGC CATGAGTATAAGATTAAAGCAGTTACTTTTGAACAGGAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTTCCCTACCCTCCCAAGGATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---			TCCTCCAGCTCTGTATCCTTGTCTGAGGGTTCTGTGTACGGCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAAGGCCAAAAGAACATACAAAGCCAGCTCTCTAGAGGCTCCA/GATCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTTCAGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---			CTCTCCCTAAGAGCCTTGGCTTGCAGCCCTTTCAGCAGGATGGAAGTCAAGACAATGAGT GGAGCCTCATGCCCTCCATGAGGAAGCCCTTAGTATTGTGACATCTGCCCTTATCCTGTCTCTCT CCCAAGTGTCTACACTTGGGCAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGTAGACC GGAAGGAAGGGCGGTCAIT/G/AGGTGATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---			GACGTGGACAAAGGAGGTTTAAATGAATACCTTGTGTG/CJCATGTTCAAAAAAGAGATTAAAT ATTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTGTCCACCACTCTTCGGGCAATGCTGCAATATCTGGGCTCAAGTGGGAGGCCACGTG GGAACAGGCCTCAGAAAAACAAGGACATGCAGCCTCCCTGAGCCAGTTCT

WI-19766b	93 A G ---	---	TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGCCAAAAGTC/G/GACAAAAGAGAAGGACACACCAAGCCTGAACCCCTC CGGACAACAGCAGAGTTACAGCTGAGGGATGCCCTGGAGTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTACCCCTCCTCTACACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCCTCAATGACTGGTACATTGGAGAAGCT/GA/JTGACAGCAGCATCCTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAAGTCAGACAACAGAGAAGGACACCAAGCCTGAACCCCTC CGGACAACAGCAGAGTTACAGCTGAGGGATGCCCTGGAGTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTACCCCTCCTCTACACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCCTCTGTTGGCTTTCGATTGTGCGATTGGAAAACCACTTGGAGAAGGGACTTTCTCTGCAA AACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGA/C/GJAAAGC TTAGAAAGGAACCTGAAATTGCTTCTTTGAATATGGATTTAGGGCGGGCGTGGGTGCGCTACGCCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGGGGTGGGATCACCTGA
WI-20512c	59 T G ---	---	CTTCCTCTGTTGGCTTTCGATTGTGCGATTGGAAAACCACTTGGAGAAGGGACTTT/GJTCCTG CAAAACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC TTAGAAAGGAACCTGAAATTGCTTCTTTGAATATGGATTTAGGGCGGGCGTGGGTGCGCTACGCCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGGGGTGGGATCACCTGA
WI-19599	230 C G ---	---	GGGCTTAAATTCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAGGATCGACCCCTTTTCC ATAACCCCTTCTACATTGGAAGAGACACACCTTGATACAGAAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAATCACAGCTAACAAACGATGATGTTGGCTCACACGTAACCAACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAGGGCA/C/GJTTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTTGAATAAAAAATTCATGGTCTTAATTGAACGTATGTTACTTTCTTTAGAATAICCTTTT TTCATTAAAAATAAT/CJCTAAACCACTCTATGTGTTCAACCTTCTGTTTAACTAAGATATGGGT TTTTGGAAGGCCACAAAGTCACCAAGCTCCATGAAGTGGCGAATTGGTCTTGTTTGGAAAGCTCTC CAGGGTGTTTCTCCAGAA
WI-19909a	29 T C ---	---	CCAGAAATAAAGCCTGAATATCTCTTTCT/CJTTAAAAATAAATTTTCTCTTTGCTCTTCCAA GTAAATCTTAAATGAACCTGTTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGGCGGG TTTTTCTTTTATACCTTGTTCTGACTGTGGAACTCACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTCTTAGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAAATGTGGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTAGCAGGA GGCAGGAAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATTTGGGTGACGTCATGC ATCCCCCATGCATTGGTTT/GC/JATGTCCTCCAGTGAGCTGTTGGGCAAGTCT

WI-20113	60	T C	---			TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGT/CIGGA AACAGTAAAGCAAAATACACACAATAGGAGGAATTTTCAGACATAGGATAATTTAAACAT CACTCAATACTGGAGCATGATCAGCAATAAATCTATTCCATAAACCAAGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATCCGTATT
WI-20895	107	G C	---			TGATGGCAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGAGTGCAGCGTGTGGC CACTTCCACACAGGAGAACACTTGACTTCATTAAAGGAAA[G/C]CTTTACTCTGTACTTTTCCCTC CCACATAGTTTAAACCCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATAACTGGTACTATAGGCAACAGATGCA
WI-20721	72	T C	---			CCTGCAATCACAAAAGTGGAACTAGTTGATATTTTGAATCATACTTGAATTAACCACTTCAGAAA TTCTA[T/C]AAACACTAGCAACTTCCCTTTATCAGA
WI-19415c	161	A G	---			CTGGATTTAATAATTTCTGGCCTAATAACCAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTCTGCTAACATGTTTGCAGATCCCTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCAT[G]AAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAGTGTGGACATACAAGGCTTACAAGTTTACACTTCTCG
WI-19348c	103	C T	---			GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAGGCGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCATGGCGTG[C/T]GCTTCTCCAGGCTCATATGGATGTCTCT CGAGGTGCACAGGGAAGTCTGCTCTGTTGTAGAAGCTTCTCC
WI-19348b	98	G A	---			GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAGGCGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCATGGC[G/A]GTGACGTCTTCTCCAGGCTCATATGGATGTCTCT CGAGGTGCACAGGGAAGTCTGCTCTGTTGTAGAAGCTTCTCC
WI-19635	98	A T	---			ATTAGTTCGTGTTGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAATAACAGTATTAT[AT]TCTTATTGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGCTGACTGCATGCAGATATGTGTGCTGAAAAGAACTTTGCCTT T
WI-19641a	46	A G	---			TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG[A/G]TATTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCTATTGATTTTGTATTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAATAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A	---			ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCT[C/A]GGGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTTGTAGGACACAAGTTTTCATGCTATTA
WI-19673b	180	C T	---			TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACCTTCTGTGTCTATGGCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGTCATCACCACTGTAAATCTAATAGT GAAAAGGCAATGATGCTCAGTATCACTGTGAAAACATTTT[C/T]CTTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACAGCTCAAAAAACACAGCCC



WI-19673a	35	G A ---				TCTGCCATGATCACATTGTGATGAAGAACAATGATG(A)JTCAGTAGTAGGTAACATTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTGCATCACCAGCTGTAAATCTAAT AGTGAAAGGCAAAATGATGCTCAGTATCAGTGTGAAACATTTTCCCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAAGCCTCAAGGTCCACACGTCGCAAAAAACACAGCCC
WI-19724	35	A G ---				TTTATTGGAAACAAAGGATTGTAATTTGGTAA(A)GJCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTTGGTTTTCTCTT
WI-19307	196	T C ---				TCCTCTCCCCCAACTAGATGATTGATCACTCTGCCACAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGGATTGCCCTCATGAGAAAATGGTGGCTGGAGTGGAGTGACATTCCTTGTCTGT GGTGAACCTGCAAGAAAGGAAACCAAGCAATGTAATCCATAGAGCCCTTTAAAGAGACCCG(T/C)TGG AAATGGGCCATGGTCTAATTTGGTGTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85	A T ---				CTTCCCTCATCCCTCTTCCACACACACCATCCCGGAACAAGTCTCCAGGATTCCTGCCACTGGC CATTTTGGAGTGTGCC(A)TJTTGGGTAGCAATGTGGAACCAACACAGGGCTTTGTGGAGAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTTGAGGGCTTTGCCACTTGTCTCATAGGGGAGCTCG ATCTCTCATCATCTGGACAGGTGGAAGCAATCTTCCGGGGCTAGGCA
WI-19946	122	C T ---				CAATGGACTGAATGAGTGCCTGCTGGTGGGTGGGGCACACACACCTTCAATACACGTCGAAGTGG CTTCCAGTTTGTAGAAAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGAGGT(C/T)CTTCCCTG ACCCAGACGCACTCACGAGCCAGTCTGTTTCAAAAATGCAATTAACCTGCGCCAGAGAGTTTCA CGTAGGCATCTTTAATAAATACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G A ---				CACAGCATGGTGTAAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCATAAATAATTATA ATAAATATACATCAAGTAACTTTACAGCACACATTTTGTAGGCCAAGTTTGGATCTGTCTGGACCT CAATGTG(A)JCTCTCGGAGAGCAGCCAGCTTAGCAGCAGATACCTTACAGCTTGTCTACTCAA GTGATGGCCCAACAGAGCTTCTGAACCTCTCTGCGGAGGTAGCTGACAAG
WI-19076	40	G A ---				TTGGTTGGATACCTGCTGGAAAAAAGCAGTTTTAATG(A)GTATTCAAAATACCTTTTAAAAA GTATTCTAGCACAAAGATTTTCTGTAACTAGATTATGTGTAAACTTTTTCTAAATCTTGTAGGAG TGTGGTTGTTAAGAACTAGAGCTTATCCTATTCCAAATCTATCTGCGCTCTGAAAAAAGTGCAGA AAGGCATTTGAAAGCTGTTCTTTAAGATATGGATTCTTTTATTCTT
WI-20218	26	T C ---				CCACACACTCTGGTTTTATAAGCTA(T/C)JAGGACAGACAGAGATGGAACCTGAAAAACAGGGTAG AAAAACATAAATTTGGAGGGGAACAGTGGGATGCAAGAAAGATGACAAACAGCCACATGTGCCCCA GTCAAATACCTTTAGTCCCTGCAGCAGAGATGCCAACCAAGTCTCTATACTGGCTGGGATCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	T G ---				CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATATCTCCAGGCTTGAATGGGAGGGGCTGGCTCTACCCCTTCTTCTTCCA TCCAGTCTATTGCCAGATG(J)CCAGAGAAAGCGGGGAGGCCAGCTCTCCAGCATAGCCACTGTGG GTCCGCTTCACTCTCTGTGACTCTCTCATGTGGACTTGTCTTTCGGGG

WI-20361a	192	A	---	---	CTGGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CTTATGCAAGATGACAGAATATGTGAAATCTGATTGTGCCAGAGTTACACTCTGCAGCTCCAAAGCTA CAACAGTCCACAGCTGAGAGGTTCCCTATACCTTCTACTACTGTGACAAATTTAGCG/AJATCCTTC AAATGGGAAATTCCTAACTACACGAGACAATGGGTCTCTACAGTAGGCCCG
WI-20572	75	A	---	---	GAGCCAAACCCAAAATAAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCT TCAGAAATTA/GJTCATAAAACATCATCTTTTACAACATGGAGAAGCGAGGTAGGCCATAATTTGTTCA AATTCATCTTTCTCAAAATTTAAATTTGTTTTAATCCCAAAGGTGCCTATTGAATTTCTTCAAAAATA AACTGCCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT
WI-20588	133	G	A	---	CATGACAAAAGACAAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAAATAGTATACAGCAATC TTCACTTTTTAAGAAAATGTGAGATCCTTTGTTGGTTTTTATTCCTTAAGTACAAAATGCTAAACI G/AJGGAGCCGAGCTCTCCGCATTACAG
WI-20593	79	A	G	---	TGACCTCATACTGGTCTGGTTAGAACACAGCCACTAGAACAACTCCAGCTTTTTCAGTCTGTTG CTGACTTTCAG/AJGTTTAAATCTGGGAATGAGCATGCAATGCTCCACAGATGAGGAAGAAA AGCTGTTAAAGGAACTCAGGATGTTGTTAGGAAGGGGAGTGATGCCAGGCCTTCACCAGACTAT CCAGAGCCATTCCATGGGTATTTGGTCTGCATACCTGTGAGACACTGAGCT
WI-19765	57	T	C	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGCTCTCAJTC/JATGTATCT TGCCCTGCTGCTTTTAGTTAGCAAGGTGTATGAATACTTTTAAAGTTTGTGTTCTTTTCCTCGT GGTATCAGTGAATACTGATCTATTCTCTGGTGGTCAATTTACAAAATTGCCATGGAACTGAGC AAAAGCCCCACGTGGGATAAAATCACTCACCATCGAGCCACCAGTATT
WI-19066i	239	A	G	---	TGACAAGGGAGAGAAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATGCTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGTGGTCAACCCTGTAGCTGAATTAATCTTCTCCATAATCCGGATGCTCAATTACAGT ACCATTCAGGGCAAACTTTTCTTAAACGCCTTCACJ/AJGTTTCTTTTAA
WI-19066g	184	C	T	---	TGACAAGGGAGAGAAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATGCTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGTGGTCAACCCTGTAGCTGAATTAATCTTCTCCATAATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACJ/TAGTTTCTTTTAA
WI-19066f	148	T	C	---	TGACAAGGGAGAGAAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATGCTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGGGTCACCCCTGTAGCTGAATTAATCTTCTCCATAATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCTTCACJ/TAGTTTCTTTTAA

WI-19066e	147 G C ---	---	TGACAGGGAGAGAGGGAAATTTACTACTTTCATTCGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTACGCTGATCCTTACGAGTCCAACTCTCTACGAGAACTGG CATATGTTCTTGCG/GCTTGGTCACCCCTGTAGCTGAATTAATCTTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066c	100 G A ---	---	TGACAGGGAGAGAGGGAAATTTACTACTTTCATTCGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCG/GATCCTTACGAGTCCAACTCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066b	87 C T ---	---	TGACAGGGAGAGAGGGAAATTTACTACTTTCATTCGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAAC/GCTTTCAGCTGATCGTCTTACGAGTCCAACTCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066a	72 C T ---	---	TGACAGGGAGAGAGGGAAATTTACTACTTTCATTCGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA/C/TTAAACCCCATGAACCTTCAGCTGATCGTCTTACGAGTCCAACTCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-20660	105 G C ---	---	TTTACAGCGAGTTTTCGCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAAGAAATGTG TGCTAAATAAAATCTCCCTTTTGAATGTATATTTG/G/GTAAAGGGAAGCATTAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATCCATCTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCGCCGCCCAAAATACTGTTTAAACACACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGGTCTCTGGCAGCCTCCCTCAGTCTTCC TCCACCGCCTCTTCCCTCCAGCCTGCCTGCATGATGTCACCCCTTG/GT/C/TTTCGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120 C T ---	---	TTCCCCAGGGTTCTGTATTGCAGTAAGCTCAATGT/GTATTTAACTTCTAGTTGCTTGTCTTTG GTCCTTCTTCCAATGATGCTTACTAGAGAAAGCAATCAGACACAAATTAGAGAAAGCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGGCAACCTGTAACTGCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-19087	37 A G ---	---	GAAAGCCAGAGATTAGCCCCGCTTCGGCATCTGTCAACCCAGGACAGAA/TTCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTGGAGATCAGAAAAATTCATATTTAAGCAAAAGTGATACAAACA CAGTGATTGGGAATGCCT
WI-18790	49 A T ---	---	AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTC/GA/GTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCTGTGCTCCTAGGCTGGACAGGATTCAGAAAGACACCAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTCAAGCCCCCTACACTCAAGGCTGAGAGGGCCTCAGGAA AGTCA
WI-18987	35 G A ---	---	

WI-18919	26 C T ---				TGGATGAAACACAGGGATTCCGGAIC/TGCCAGACCCCAATTTATACCTTCTCTACAGTG TTGTTTGTGTTGTTGTTTATTTTATACCTTGGCCATACCAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A ---				CTTTCTGGTCAAGGCTTGGACATCTCTCAGTCATCAGACAGATATCTCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTAATATGAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38 G C ---				CTTTCTGGTCAAGGCTTGGACATCTCTCAGTCATCAGACAGATATCTCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTAATATGAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23 T G ---				CTTTCTGGTCAAGGCTTGGACAT/GCTCTTCAGTCATCAGACAGATATCTCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTAATATGAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170 G A ---				TCAGAAAGCAGACATGGCATCTGTTCTTCTGCTTGGTTGTTGTACCTTTACGAGACCTGAAT TTAGAATTGCCAGTCTGCCAGAGTGAAGTGAATTTCTCTTTCAAGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTCAATAACATATCAACCA[G/A]TAGCATTAAACCAATTTATTTCCCTGCTCT AGTGCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCGAGCATGCT
WI-19212	46 T A ---				CCAAAGTTGCATCCATGTTTGAATTTCTGATGAGACTAGAGTGACAGT[A]GTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATATGCAGATGGCCTATGGAATGACGTGC ATAATTAAACACATTATCAAGTCTCTTACAAATTTATTTCCGAGCATGTCAGTAAAGTAGACCCA ATGGGAGAGAAATGCCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210 G C ---				CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCTAGACAGGTAAGACACACATTGGATG GCAGCATGGTTCTTCCCATTTATGGCATGAAATATGTGGTTAGAATAAGGAACAGCATTAAT CCTTGCCAAACAGCCTCACTAAGAGGCTTTTGTCTGAGTCAAGCAACACATTGCTGCTCTGCCC CTTGGAG[G/C]TGCAATTTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214 T C ---				TTGAAATCCAGTCTCTGCCCCCAGGCGGCTGTGCACCATAGATGTCTTCTCTACTGGGTC GTTCTGGCTTTTGTAGAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAAGACAATGTTTCTGTAATCTGAAACTGGAACCTGAACCAAGTTTGCCTTCTCCTAGTCACC AAGCATACTT[C]TCTGCTGCTCCCCAAGTACTTAATGTTCTCATCTGT
WI-19041	198 T C ---				GTCTCCCCAGAGTCTCTGCACCCAGCCCTGTCTGCTGTAAAGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCCAGGGGGTGCCCTTAGTTGGACATGCTGGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCAAGCTCATCACACAGGGGCCATCCTTCTCAATACAGCC[T/C]G CCCTGCACTCCCTATTTCAAAATAAAATAGTGTTGCTTGGCTGCTGTGT
WI-19135	20 G A ---				CAGTTACCTGCTTTGCCTC[G/A]AAGTGTCAATCAATTTGTAATTTAGTATTAACCTCTGTAAGT GTCTGTAGGTACGTTTTATATTATAAGGACAGACCAAAATCAACCTATCAAGGCTTCAAAAAGT TTGGGAAAGGGTGGATTAAAGTACAGCAGATTGGCTTACAGTAAATGAAGTATTTTATTAAC GCTTTGCCCATATAAAATGCTGATATTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54 G A ---	---	TACACAGAGGGTGCACCTTGGACTCTGAGGGTGGGTGTGGAAGGGGGAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCTGTGAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTTAGGGAGGT CACCTTACCCTTTTTCATAGGGAAGAGTGTACACTCTCGGTATCTCAGGGGAATGGGAAAG AATCTTCAAGGGCAAGAACTCGTGGGAGGATGCTGTGTATGTAATACT
WI-19144	222 G C ---	---	GTGCCAGTCTTCCAGAAAGCAAGACTGCCCTTCATTACGCCCTGCTGACCTCCAGCCCTTCTAAGG CTCAGCCACAGGACTCTGTGGCTGCCAGCTGTGAGCTATCTATATTCATTATCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGAGGCTGTGCCAGGAACCCCTCTCTCCCTGGT CTGGCTCTGCTGGAGCGG[G/C]TGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110 C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCTGACAGAGTGGGTGGCAGACAACACTAG[C/A]ATTTACGGGTGTGGGCAC ATGGGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66 C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA[ C/T]GGCAGATGCCTGACAGAGTGGGTGGCAGACAACACTAGCATTTCACGGGTGTGGGCAC ATGGGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112 T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAAGGGTGCCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTG[C/G]GGCTCATGGCAGAGCATT CAGTGCCACGGTTTAGG
WI-19235	173 A G ---	---	TCAGGAGGTGGAGTTGCTGCTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTGTAGCTTCTCTTCACTGCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCCCTGT CACTCATGCCCTTGCCTAATGTTCAACAATGGTGGAA[G/G]GCTTCATGTAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCAGCACTA
WI-19222	179 C T ---	---	CGTTTTCCCTAACTACCCAGTTTAGTTGGGATGATTTGATTTCTGTTGTTGATCCCATTTCTAA CTTGGAATTGTGAGCCTCTATGTTTCTGTAGGTGAGTGTGGGTTTTTCCCCCACCAGGAAGT GGCAGATCCCTCTTCTCCCTAAAGGACTCTGCGGAAC[C/T]TTCACACCTCTTCTCAGGGAC GGGGCAGGTGTGTGTGAGTACACTGACGTGTCCAGAAAGCAGCACTT
WI-19117	134 A G ---	---	AAATAATGCAACGCGAGGAGGAGAAAGAAATGCACCTAAGACAAGAACATCTCTCATAGAACATTG ATCTGTTTACAGGAAACAACCTTGCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA A[G/G]TAGCTATTTTTTCCTAAGACATTTTTCATTCATGAATATTTTCAAGTTTTTCATACTGTACA CATTTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTTG

WI-19134c	263	C T ---	---	CTCCTGTTCTGTGACCTGACAGGGTGACACAGCCCTTTCACACTCTGTCTCTCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCCAAGAGGGGTGACGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGCAGCAGCTGCACTATCCTTTTCAGAGCAC TTCATCCACTTGTCTCTCTCTACCTCGGCACCTGGGTGGGAAAGGG
WI-19134a	162	T C ---	---	CTCCTGTTCTGTGACCTGACAGGGTGACACAGCCCTTTCACACTCTGTCTCTCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCCAAGAGGGGTGACGCCAGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGCAGCAGCTGCACTATCCTTTTCAGAG CACTTCATCCACTTGTCTCTCTCTACCTCGGCACCTGGGTGGGAA
WI-19224	112	C T ---	---	GGTTTCACCACTGCTTCCAGGGAACCTCCGATGAAGTGTCCAAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAAACAGAGGAGATAATCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTTATAATCCAGCAGGCCAGAAAGACTTCC AGGGAACACTCATTCAGGAGGTGAAATGATGATGACTCCTCCAAGATGAAAA
WI-19201	179	T C ---	---	GCAGTCTTAAGGACCACTGGCCATTAGCTCTTGCTTTTGATGGCATTCTTTCCACCTTGCTTCTC CTTGTCTCTCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCGGCCCCCACACTTTCCTGCGAGGTGACCCGAAGGACCTCTGGGGGATAAAATTCAAAAA GTGTGATGTCTGCTCAGAAAGTCAAGACTCCATGTCTGCTGGCTCAAA
WI-19034	45	T C ---	---	GAAATGGCTCCACTCAGAGCTACCCGGTGATGAGGATAGGGGAATCTCCTCTTATACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTTGAAGTGAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTCAGCATTAAAGTCTGTGCGAATTGAC ATTGCTACTTATAAATAGTCCCTAAGTCTTCTTATGCTGCTATATA
WI-19102	25	C G ---	---	TGTTCTGAGTCACGCTGAGGAGAGCTGCTTCACTCAGGAGTTCATGCTGAGATGATGATGATTCA TGCGACGTATATTTCCCTTTGGAAACAGAAATGAAGCAGAGGAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGGCTAGAACTCCTGTAAAGTTTGAACCTCAAGGAGAGGATAT AGTGAATGAGTGTGAGCATCGGGCTTTGCAAGTCCCATAGAACAGAAATGGG
WI-18548b	65	A G ---	---	AAAGGAGGGAGAAATCTTTTACATAAATGCCCTTGATCATCTCCAGTCCCTCACTGGGGAA[V GJAAAAGCATCTNTCAAGTCTTTGICCAACTTTGGCTGC
WI-18548a	62	G A ---	---	AAAGGAGGGAGAAATCTTTTACATAAATGCCCTTGATCATCTCCAGTCCCTCACTGGGG[G/AJA AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	T C ---	---	GGCAGCAGCTTTTAAATTTGAACACTTCTCTTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTT[CJAAGATCCACAATTCAAAGGCCACTGCTGGCTCA CTTCCTCACA
WI-18501	121	C T ---	---	CAGAGGGAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCGNACAGCTGAACCTCGCGCAGGACAGAGGGGG[C/TJGACAGCA GCGCATGCCACAAACATTCA

WI-18017	87	C A ---			ACAAAGAAAAATGGAATAGGTTTGGAAAACTTATCTGCTGTACAAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA/C/AJACTGCTGGATAAATCGTTTCAATTAATATATCTCTTTGCAT CAGAGCTGGTGAATCAT
WI-18148b	101	A G ---			TTATTGGTTCCTTCGATAAACCCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAAACGAAAGCA GTGATTTTCAGAAACNCGATTCTGAATATCCG/AJGTGGCGGCATATGCAAAAGGAGATGA
					TATACGGATCATGTATTGTGTGACCAACCACCTACACAGTCAATTTGTAGAGCAGTTAAATCAC/T/C JGCCAAAATCCCTCTTGCCTTCTGTAGTCAGTCCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCGGTTCCTAGACATTT
WI-18254	64	T C ---			CAAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAAGACGGCTTCTGGCCNCTCTGCGTCC AAGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG/C/AJGTTTTCAACCTTTC CTTGGGTGTTCTTCAG
WI-18265b	117	C A ---			ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG/C/TJTTGGGAAGTAAAGTTGATTACT TCCTCTCCAAGGATGATATGTTAATGAATCCCTTTNCCITTAGCTTCAATCTTCAATAATGCCAAA
WI-18295	40	C T ---			GGGCAAGAGACAGAGATTTAATTGAATAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT/ CJGAGTAATTAACAACATAATATTTANATGACAGTGCAATTAATAACGTCCTGGGTAAAGCCAGAG GGGAGAGAGGGCTCTTCA
WI-18459b	64	T C ---			TTTATTTTAAATTTGCATCCTGAGATAATAAAATTTATCTGACAAAGTGAACAATG/AJG/CAGAAAGC AGCAGTGAAGATTTTCGGAGAGGAGGTATCCTTCATTTTGGACAGCTGTATATAGATTGA
WI-22585	56	A G ---			GGGCTGTGGAGTAACAGAACTTGATGGAAAATTTGGC/AJGJCTGTGTAGAATGATTTCTAAAGCTTTC AGACAAATGGCAGA
WI-21155	36	A G ---			GCCTTGTCTCTTGTCTCAGAGGCCCTCAGATGGATACGACGCACTTCTTTGAACCTTTTAT TTTCTCGCAGGAAGAAG/AJGGATCCAGCAGTGAGATCAGGAGGTTCTGTGTTGCACAGACAG GGAAACAGGC
STS-F02766b	88	G A ---			GGCAGGATTCACCCATAACAGAGAAATACTCCTTATTGGAAACAAGGTTTTATTTTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTG/AJCTTGGACAAACGTTGTAAAGATATTAATGCCACT GAACTGTTTCATTTAAATGGTAATTTTCATGTTATGTGTATTTCACTCAATTAAGAATGGAACATGT CTTATAATTGTAATTTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-19888a	98	C T ---			TGAGACCATCCTCCTCAACAAAGAAATCAGTCAGTTCAGCACCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAG/AJCTTGTGCACACAGTACAGTGCACAAAATCCAGAGGGCAACACATTGTAATT CATATCATCGTTTCCAAA
WI-21485	82	C T ---			
WI-20601a	125	T C ---			TCAGAAATGCTTTCCTGCCCCCAACCAAGAAATTTAATGAATGONCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCTTGGAGGTTGATGACAGGATTAGTCTCTGTGTT/CJCTTGGT GCAAGTTTGAACCAAGTATTATGTACCATTCATGACAGAGCATCTGTTTCCCTGTGATGCCCACTAG

WI- 20561b	94 T C ---				CGTTGCTTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTATG TACTTCAGATGAAAAATCCTTACATGTC/C/GGAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---				CGTTGCTTATTAAAGATGGCTGTTT[A/G]TAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTA TTGACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---				GCTTTCATTTCTGTACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT AT/A]ATAAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGCTGCAATTTCCCGAGATAA
WI- 20116c	59 T A ---				GCTTTCATTTCTGTACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTT[A/J]TAGAA CATATATAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGCTGCAATTTCCCGAGATAA
WI- 20116a	22 C G ---				GCTTTCATTTCTGTACCCAC/C/G]CTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGCTGCAATTTCCCGAGATAA
WI- 20466b	133 G A ---				AAAGATTGCAGTCTGGGACACAGTTTGGAAAAACACTATTTATAAGTTGGCCATATTACAAACAG NTCCCAAATGGTGAAACTGGTATTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC G/AJTGGAACATAATGTTTAAAAAGTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTTATCCCTTTCAGGTTTCGATT
WI- 21444	39 A G ---				CTGGCAGCAAGTAACCAATTTTAAAGAAATACTCTCAAC[A/G]AGTTCTTTTATGCGGTTATTTCA GTTGTTAACAAAGTTAAATACCTATTGGAACATACTTTTGTATTATTTCGAGGAAGAAGAACTCT ATAAGATTGACTTACTCATTGTTGACTGGTTTGTGAGCCTTACTGGG
WI- 21034b	148 T C ---				AGAATGGACAATGATGAGATGATTGTGAGCATTGTGAGAAAGTGGTATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAATTACTGGTCATGG GAGATTGGATAGAT/C]GCTTAACCTATCTCAATTTTAAGTAATGTGAGCAA
WI- 22091c	205 G A ---				GGGTGATTTTATGCAATGTCCAAACCAGTCAAGCTATCATTTGAAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCATGTAACATACAAGCATATTACCTCCCCCTTAAGTACTCATTAATTC ATTACTTGTGTAGCTTTTAAAGGTTTAAAAATGTTAGCATTAAGTGGTATTACTTGAGGGCA ACA[G/A]AATACGGCTTAAACACACACTAAATCATGAGGCTCAGGGATTG



WI- 21805a	45 A T ---	---	CAACTGCTGAGGCTTTCTACCTAGCTGATTTATAATCCTATATT[AT]AAAAAAATCTATAGTCTG CAGTCTTTGACATACCTTCTCAAGGGTGGATATGTTGGTGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGTCTTTTGTAGCTTAAGTCTGTTTGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCAATAAATCGAACAGTTGAAGGCTGTTTGTGTAATTGCTG
WI- 21778b	155 T C ---	---	AAAAATCCATAATTATTGAAACCCAAAGTTACAGAGAAAGTTTCGTAACCTTTTATTGAATTATTGAC TCTGCCCGCTGTCGTCGCTTCACTCCAGTCTGTCATGCCCTGTGTAGGTGGGTCCCCCAG GTCTGGGCTTCTGAGGTCTGTCGTTGCTAGAAAGGAGGGCAGGTTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGTGATGAGGCGAGTTCGCTCAGCTGCAGTCCCTGACTCCGGAACACTGTGCTCT CAAATGATCTAGAGCTCATCTTGGCGGTACATGAGGGCAGTTGTTGTTCTAGTACCCATTAGCCC ATGGCTCTCAAGCCAAATTCACACTGGGAAAAACACACCTCACAAGATGCCATCCATTGAGTTT ATACAGGTTTGTAGCTAGAACTAAAAAACATTTTAA[C]AATATCTA
WI- 21449b	222 C T ---	---	AACAGCAGCAGTCACTTCCAAATGCAAAAAAATTACAATTTTAGAATAAAATTATAATGTTTA TAATGCGGGTCAAGANTTGAAGGTACAACAGAAATCAATCACGCAGCACTGGAGCGGCTGGAG AAGCCAAAGCCCACTGTGTCAGGGTCCAAAGCTGACAAGAAGTCCCAACCTGAGAGGTCTCCACACC AAATCATACCCCTCAGCTTCCCA[C]TTTGACAGAGCCAGTGTCTCTGGGTTAG
WI- 21558a	157 G A ---	---	GCCTACAAAGGAAGCCTGTGGACAGCGAGNTGGTGGAAACCGACTCCAGCTGGAAACCTGCCCTC CCATCCCCCTTAGCGCTTCTGGCCCTCCGGCTGATTTCTTCGACAGAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGGCAGTATG[A]AGCCAGGGACTCCCTCCACACAGATGAGGCCCTAGGGCTGCAA AAGGGCCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI- 22187b	178 G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGCTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGCCCTGACCAATGGGTGATTACATTTAAAAACCAAAACCAAAACAAAAATACCAAGA ACAGATCACTTGGCATGGACATCAGTAATCTATTGGTAATGGT[G]A/AAATTTTCATGAAAAATTTCC CCTAAACCATACAAAAACTGTCTCTCTACCCCAAAAGTGTGGAGGAAAG
WI- 22187a	110 C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGCTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGCCCTGACCAATGGGTGATTACATTTAAAAACCAAA[C]A/CAAAACAAAAATACCA AGAACAGATCACTTGGCATGGACATCAGTAATCTATTGGTAATGGTGGAAATTTTCATGAAAAATTTCC CCTAAACCATACAAAAACTGTCTCTCTACCCCAAAAGTGTGGAGGAAAG
WI- 21609b	146 G A ---	---	TCATGAATATGACGCTCCATAATCTTCTCCCTTGTAACAAACGTGCAGTCCGTTTCAAGCTGTAAA AACAGCCCCAAACCAAGACATCACAAGAGGCAAGAGCAGTGGCAGTGAGAAGGGAGCCTGTAAAG GATGTTTCAAG[G]A/JAGGGTCCCGGCTATGTGGCCCACTGGATGTAGGCAGTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	---	TCATGAATATGCAGCCTCCATAATCTCTCCCTTGTAACAA/C/JGTGCAGTCCGTTTCAACAGCTGT AAAAAAGCCCCAAACCAAGACATCACAAGAGGCAAGAGCAGTGGCAGTGAAGAGGGAGCCTGT AAGGATGTTTCAAGAGGGTCCCGCTATGTGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	---	ACATCCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCTTTGTGATCTGT/GJACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACAGTCTAAGGGCAGGCAGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTGACAGGG TTTC/GJTGCACTGGTACAGAACACACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGG/JATGTGACAG GGGTTTCATGCACCTGGTACAGAACACACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	---	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG/A/GJTTTCA TCATACAAGACAAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	---	ACAACATGCCTGTTACAGGGGGAAAAATCCTAGG/JAATAACTTATGTGTACTTCTTGATTCTCA TCATACAAGACAAAGCACAAAAGCACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	---	AGCCAACTCAAGGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA/GJAGACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTAA AAGAATACTAAGATTAGATGAACACAACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAAGGAAC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	---	CTCTGAACCTAAAGGGCCGTGAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCAAT/AJACAT TGGCTGGAATGAGGTGGTCAGGAAAAATAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAGTGAATAATTACAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTCTCCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI- 22130b	165 C T ---	---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCCTTCCCTCTCTCTGACAC CAGCAAGGGGGAGGCCACCATCACGGGCCCTGCCCATCATGCATCCAAATGATTACTAGCTAGGAA GCCAACGGAANAGACCCCGCGCTTGC/JGTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGCTGATGGGAATGAC

WI-21661	117	G C ---	---	---	GCCTTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGTCTTTCCAACTTTAGAATGTATAAATAAGAAATGACATTTTAAAAATAAATAA(G/C)TTTAGTCACAGTCAACAAAACTACCTTCTAAGGAAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTTCAGCTATGAAGGA
WI-21980a	25	T C ---	---	---	GA TCAGTTAAACACATTCATCAAGGAT(C)JAGATTAAATTAATGTCAAGGTGAGCATAAAAGGGAGATTATAAACAGAAATGTGTTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTTATTAATTTTCATGGGTGAAGCCCTGGGATAAAG
WI-21636	71	A G ---	---	---	TGCTTGATTAAATGTGGTGTACATTATCCTATTTCACAGATGGAACACAGAAAATACCAGCTTTTTTAAAJ(G)TAGCAATATCTATTATTAATAAATAATTGAAATAACACCATATAATAATACATAAGGAAGTAATCTAATTGTGTTGATTTTCAGAGGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGCTCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGACAGGGATTTC
WI-22457a	112	G A ---	---	---	TTGCTATAATTTCCTTAAAAATGCAAAGAGTACATCACAGCAGAGTATAGCCAACTCACTATTAGACAAACAGTAACATACCTGGACACGGTTTCAGGCATGAAGGATACA(G/A)CAGTTAATTAACATAAAGGAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAAATACCTGGGGCCAAAACCCACTGAACCTCACCCAGCTGAAACACATGAAGGATACCTGGGTAAAGGA
WI-21524b	97	C T ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATACTTAATGGTTAATAACAGCATTCCTGTCTACCCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTTCTCCAAAGTTACTTCTCCAGGGGATG
WI-21524a	35	A C ---	---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATJ(C)GCCGTGATGTACGACCTTCGCGTCATACTATAATGGTTAATAACAGCATTCCTGTCTACCCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTTCTCCAAAGTTACTTCTCCAGGGGATG
WI-22652a	32	G T ---	---	---	TTACCTTCCAAAACCCAGGCCACTTTGGAGAAAG(G/T)AAGAGAAATGCTATTAAATCAATAAGCCAAAGACAATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACACCATCATCTCTGCCACAGAACCCTTGCCACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTTCTTTAGGG
WI-21703d	197	A G ---	---	---	CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGTGGTGGTCTGGGAGGGGCTCTGCATCCCTTTCTCAGCACAGACCATCTTCAACCTCCTGGGAAAGCAGCATTTGGAGCCTACACCACTTGTGCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAJ(A/G)GTGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTTGGGGGAAGAG



WI-22724	117 A G ---	---	---	TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGAAGTGTAGAGATATAGGA CAAAATCAAGATTGTCAAAATGTATAGTAAGCTGTTAAAGCTTGCTAAGGGT[A/G]TATTCTATTTT TGGGATATGTTGGGAAT
WI-22750	48 G A ---	---	---	TGTAACCTGTGTTTCTGAAAGTTGAGGAAAGCTGAGGCAGCTAATG[A/G]GCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTGAGCATCTGACCATCTGACTGTGCT
WI-22775a	60 A G ---	---	---	TGCTGTTCTTTAGTTTCATGACGTTTATCAAAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAGGGAAATAAACTCCCTAAGGGCAGCAATAATTTCTGCTTTGAATCCCTTCATTGAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACCTGAGGTATGAGGTGTTGGGAGGCCAGGAAAGGAAG GGT
WI-22808	143 C T ---	---	---	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAGAGAGTAGGTATAAGAACCAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207 G A ---	---	---	TCCTCGTGTCTTGAGCCCTCATCCCAACCCCTCCAAGCCCTCATGCCACACACCGTGTCACACATT CCCCATCCTCCCTGTCTGCCATCTCAAGTCCAAATCCAAAGCCAGAGCCCTGGCAGCTTTCTCTG GGAGACAGATGAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGCGCTGTGGGTG CT[G/A]TTGGCGTGGTGAATGAGGGGCAATCCTGAGGCCAGAGTTCA
WI-21031	31 C T ---	---	---	TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCAATTTGCTCCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122 A T ---	---	---	CCATATCCAGTCTCTTTGAAGCTTTCTATTGACITTTAGGGTCAGTTATTATATCCTTTATCACTAT GACTTTCATTTGATTTTATTTGTTCTTCCATTTCTCTGTCAAACITTTCT[A/T]TTTGTATTATAA ACTGTTTCTAAACITTCACCTTAATCTCTATCTGTATTNCTGTAGTCCCTGAACITCTTTTAGAGG
WI-21186	95 G A ---	---	---	AGCGAGCATCAGAATCAGCTAGAGGGTTGACTAAACAGACTTCTGGACCCACCCCCAGAGCTTCT GATTCAGTAGGCTGAGGTGGGGCTTAC[G/A]AATTAGTATTCGAAGACCTTCCTAAGTGTGCAG ATGCTGCTTGTCCGGGGAACACACTTTGAGAACTATTGTTCTAAAATGTTCTCTCTCTTTTAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATAATGTTAAT
WI-21187a	94 A G ---	---	---	CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAATCAAAATACATAATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GGNCTCAGTAATGCTGTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCAATTTGCATCACCTAGGGGAATGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---	---	---	TTTTCCCATACCAATGCACCTGTTGTATAACTATT/CJGTGGGTAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATATTATTAACAATAATTAATAATCTGTACTATTACTGC TTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTATTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 G A ---	---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTGTTCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCAATTCGCTCAGGAAGAA
WI-19937c	185 C T ---	---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTGTTCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCAATTCGCTCAGGAAGAA
WI-21117b	227 C T ---	---	---	GAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCACTGAAATCTGTTTCAGTTTCACAGGCTC TCTCCAGAAAATGCATATGTACCAATTTGCATGTACAATTTAGAGCCTTCAAAATACATTTCTGGGG TCCAATCACATCTTCAGGTTGAGACTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATTTC/TCTACTGAAATCTGGGTGGGAG
WI-21122a	42 C T ---	---	---	TCACCTTTGATCATAATCCCTGTAAAGCTAAAGTTATCA/C/TJTAACAGGAACCTCTGTTTTCC TTATTCAAATGTACAAGCCTGACGCTTACTGTACATATTGCTAGCAGGAGACAACCTGGAAATACT AAACAAATCTGGAATTCACATTTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTGTTGGGTGCT
WI-21254	53 A G ---	---	---	CAGTTTGGTACAGGAAGGGCCCATGAATGTGGGCGGAACCTATCCACAGGAG[A/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	---	AAGGAACTGCATGGGTACAAATG/TJCCAATTCATACTTAACAAGGTGGGAAACGGGTCAATCT TGGCCTGCTCCAGAACAGGGGCGAGTCTATGCACTCTG
WI-21059b	181 T C ---	---	---	GGGACAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGCTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGAAGAGACATACCTCACTGAAGTCATTTCTCTATTCT/JATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCTTGCCTAAT
WI-21059a	63 C T ---	---	---	GGGACAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGCTTGCATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGAAGAGACATACCTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCTTGCCTAAT

WI-20442	37 T C ---			---	TCCACGTGAAGGAAGAAAAAANGGGGGGGGCTT/CJTAAAGGTGGCACAATTTTAAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAACACAAAAGTCAAGTGATGAGACGAA CA
WI-21235	43 T C ---			---	GTGCAAGAGGTGAAGCAAGGGACAAGGGCAGCAGGGCAGT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---			---	ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGAATGCCTACATCTGGAATTT/CJCATTAAC ATCAACGTTAAATTTGTCCGACCAGTCTTCATTTGCTGATCACTTTTGATAATGACAGATCCAAACAT GAACTCCTGAAGCAAAATGAATATTACCTTGCTTTTCATGCAAAATTTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAAGATCTAAGGAATTTGTGACAGGGATCTTCT
WI-21149a	167 G A ---			---	AGGACCTGCTCTCACACGTTCCCTACCCCAACAGCTTTTGGCAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTTTTTTTTTAAACAATGACCTTATTTATCTTTTAACTTAAGTCTTATATA CAGACCTGCCCAACTGGAAAGCTTTTACAC/GAJTGCTTCAGAAATGCGGCAGTATGACACAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-21376b	188 A G ---			---	GGTGCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAAGGAAAAACATTTCAATGTGTC TTCCATTTGATGAATTTGTTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAAACCA GACAGTGAATCTGTTCCAGCCCAATCTGCAGCAATAGGAGTATGAGTCTC/A/GJGAAAGTGATTTCT GAACTGAGCAGCACTCATGTCTGCATGGGAACCTCTGGGGAGAGAGCCT
WI-21382d	125 C G ---			---	CCATTGCAGTCCAGAGATGAGAACTGGACCAGAGGCAATCATGAACAGAACGGGAGTCAAGAGA AGGGGTTTCTAAGATGAGAAAGTGGGGGGGTTTGGATCCAGTGGGATNGGCTTCCCTC/GJAGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCAGTCTGATGGGGAGCAGAAAGAGTGCCTCATCCTC AGTCAGGTCGAGTCAGGTCGAGGAGAGCTGCTGCTCCATAGTCTCGCAC
WI-21437a	201 G A ---			---	TCCTGAGGTTGGAGTCTAGCATAGCTCCCTCCCTCAAGAGGACAAGGGTCAGGGGGCAGAGC AAAAATCCAGTCTCTCAACCAAGGAGACTGCCCTTTGGGATGGAAGTTTCTGGAGCTCCCTCCAT CTATTCTGTGGGAGGAAACATGCCAGGGCTGCTGGTAAATGGCAGGGTCACTTTACCAGGGGQ/G /AJCAGGCATAGTGTGGCCCTGCTGCTGGGGGGCCACCTGGGAACAGT
WI-21202b	156 A C ---			---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTATTTCTGTAAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAATGGTCACATATATTTTAAAGTAACTGATTTATTGAGGG AGGAGGAGAGAGTTGACCAAJ/CJGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A
WI-21202a	61 T C ---			---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTT/CJTG TCTGTTTTATGAACATGATTTTATAAAATGGTCACATATATTTTAAAGTAACTGATTTATTGA GGGAGGAGGAGAGTTGACCAAGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---				GCATGAAAGAACTCCAAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAA/GJTCCAAAGTCATCTAATTAACCATATTTACATAATTTGTAGG GACAGTATACTACTCTACAATAAATAAGGGTTTAAAAAIGTGTCTTA
WI-21627a	106 A G ---				GCATGAAAGAACTCCAAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC/GJTTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATTAACCATATTTACATAATTTGTAGG GACAGTATACTACTCTACAATAAATAAGGGTTTAAAAATGTGTCTTA
WI-21399a	75 C T ---				GGATTTGAGTCCCAACTTGATCTCAAAATTCACCTTCTTGATGTAACAAGCTCATTCCTCTAAAGTT TCAGTTTCTTTTACCAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATGCTTGGTAA CTGCCTCTGCAATTTGCTCTGAGGTGTGTGCTCCCTAGGACTAGGTAGGATCTCTCTGCTTCTGCC TTACCTAGGCATAGTGCTGATAGCAGGCTGAAGCCCCAATTCATCTGT
WI-20329a	68 G A ---				CGATGCTGCTAAGATAGGAGGTTAAATCTTTACATGTTGAGTGGTCCACAGACAGACATCAAT C/GAJTCTGTAGCAGCGAGAGAGACACTTTAAGTTGCCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTCTGGCTTCTTAAAAACAGTAAACCAATCAAAAAGAAAGATTAGAGGTTTACAGACATT AGGAACAANTGTGGCCAGAGATACACAGAGCCCTTGAAGGAAAGGCCCTCACT
WI-21249	155 T C ---				TTCTGGCATTCAAATGTACATGTAATAATCCAATTTAACAGATCAAAATTTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACTTTTAAAGAAACATTATAAAGGTAATT AAAACTCTAGGTGTATCTTAT/CJATGGAACTAGTTTATTTCCNATTTAACTACTGTTTCATTGGGTA AAGTATGTTGCCCAATTTTCAGCTGTTTAAAGGAATTTATAAACAATTGAGA
WI-21504	147 C T ---				TGACACAGCATCAATTTTCATGAATACTTTGAAGGGCCATTAGAAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCAATACAGTGGGGGCACGGGCCGTTCCGGCTCCAGCTGGGTTTCCC AGATGCAACAAT/CJTGCGGTTCTGGCTTCTCCACTGGTGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---				CTGCACAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAACCGCGGGCAGGGAGGGCAGAGAAC/GAJCACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181 A G ---				TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGACGTTGGCCCTGATGTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTCACTTCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGACAGTGCCTTTTGGAGAAAGGCA/GJAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCGTTCTCCACCCTATTCTCTCCCTGAAAG



WI-21475b	117 A T ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGCCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTGATCTTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGCAGTGGCTTTGGAGAAGGCCAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTCCCGTTCTCCACCCTATTCTCCCTGAAG
WI-20893d	207 A G ---	---	TGTTTGTTCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAGGG CTGCTTCGGCGTTTAAAGTCTACTGAGGAATACAAATCATTTGTCACGTAAAGTTACATCCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTCAGIACATAACATTTGGTAGAGTAAACAACAACCAACCAAGCCTAAATG
WI-20893c	179 T C ---	---	TGTTTGTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTGCAGGG CTGCTTCGGCGTTTAAAGTCTACTGAGGAATACAAATCATTTGTCACGTAAAGTTACATCCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTTGGTAGAGTAAACAACAACCAACCAAGCCTAAATG
WI-19941c	71 C G ---	---	GAGCTCAAGGGAAGACCCCTTACCCAGATAGGACTAACTGGAGGGTGGAGGGAACCAAGGTGAAA GGTATTCGGTCTGTGAGACAAAGCAGGGGGCTGAGAACACAGACAGCAAGGTGGTTTGGAG GGACACAGAGGGTGCAGGAAGGAGATGGGGACATTTCTTATCCAGTGCATGCCCTTAAAT AACTGGGTACAGGAGCATTTTGAAGGAGAACCAAGGACAGACAAAGCG
WI-21552b	166 C A ---	---	TGGGTACATGGACAGATGATATGTTTATGGGTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATCGGATCTCTTCACTCAAGCATTTATCCATAGTGTACAAAGAA TCCAAGTATACTCTTGATTTTAAATGTA/C/AJAATTAAATTTATTGAAATTTAGTTACCCCA ATTGTGCTATCAAAATATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI-21552a	66 G A ---	---	TGGGTACATGGACAGATGATATGTTTATGGGTATATGAGATATTTGATACAGATACACAATGTG /AJAATAATTACTTCAGAGTAAATCGGATCTCTTCACTCAAGCATTTATCCATAGTGTACAAAG AATCCAAGTATACTCTTGATTTTAAATGTAACAATTAATTTATTGAAATTTAGTTACCCCA TTGTGCTATCAAAATATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAATATTTCTGTTC/GTAGAGAGGA AAGAGCTGGTCCCTGCTGAGGCAACGTCAGGTCGGGGAAGGCACCTCGTGGTCTGTGATCTGTC TCAGTATGGGAGGCTCCACTCGCCCAACAGGCGAGCTCGGGCCAGAGATGAGAAATATGCTGTAA TCCAGTACAGGGGCTGCTGTGGGGTCCCAACAGCTCTCTTTGGGGG
WI-21513b	192 G A ---	---	CACATAGTTTCTCAAGAAGAGGATGAACGTGAACCTTAAAGGAGCAACAAAGCAACTTTCCATT ATTCTTAGTTTAGACCAGAATCTTTAAATTTATTTATCTCTTTAACTGTCAAAATACACCAATA CTTAGAGGAAATATTCACAGTATACCAAAACATTTTAAAGATAAAGAGGCGAGTGAAG/AJAGTAG TATTCTACATACCACAGTATACAATGATGCCCTTCTGCAAGGTTTAGGAAC

WI-21514b	133 C T ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAGGACGACATTACCATGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAATCTCCTTATGCAGGAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGAITTTGTCAAGGGTCATAAGGAACT
WI-21514a	100 A G ---	---	TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCAAG/GTCTTCAAGGAAGGACGACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAATCTCCTTATGCAGGAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGAITTTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---	---	ATGAACATGTTGCAGTGGGATGAAT[C/G]TTATCATGCTAAGTGAATAAGCCAGACACAAAA AATCCAATGTATCATTTACCTGTATGAGGGTACTT
WI-19576a	113 A G ---	---	TTCATCGGTTCTTAATACAGTACAATCCTTTTGTGTAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACTT[C/A/G]TCTAGTTCAGTGATTAGT CACAGAAITTAACATCTGCCAGATGTACACAATTTGGTAAAAAAGTACAGCTTCTCTCCACGGGGA G
WI-21695a	141 A C ---	---	ATACACAGGCCACAATTGCAGGATGGAAAGGCGAGTGGGCACCTTGGAAAGTGACTACACATGGCAATA AGCAGCCTATCTTCTTACCACCAAGAGTTCTTGGGCGATGTGATGGCCAGACCCCTTTCCAA GGGAATA/C]T]ACTACACTAAGCCTACACTGTACTGTGAGAGTCATGGTGAACAAGGCCACAGGC AGTGGGAGGAATGTGATGACTTCACTGTGTTTCAGANTTCTAAGGCCACAGCAT
WI-21574a	235 C T ---	---	AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAACCTCACTACTAGGAAGCAACTTATAGTG TGTAATATTGATCTAGCAGCAACTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTGTGAATGTCCTCAGAGTCAGTGGGAGCCATT GGGCAGGCCAGGGAACCTTACTGCTACTTCTTCTTCTGTCAGGTGGGA
WI-21644c	151 T A ---	---	TGACTGCCAAGATTTAGGCCCCAAGTTCAGGCAAGGGTCACCTCTAACCTTTCAGGAAGCTTGGGT GTGACCCACTGCATAAATGGATTTTCCACATANTATTACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGAT/ATTCATCAAGATCCATGGAATGATGCAGTTTAAACATGTGTCTCAGC TTGCCTACTGACCACCTTCTTTTCTAAATATGGCAACAGCACAGCAAGTC
WI-21614b	55 G A ---	---	TGCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC[G/A]TTTTAACA AACCTCATATGATCACTGTGCAATTTTCAGTCACTAAATACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGTATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCGAGTTGGCTGTGTGGG
WI-21615b	151 C T ---	---	GACCGAGAAAAAAGTCAAGGCATATGATGTTTGTGCAAGTATCAGTACTTTCAGGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTCATACATATTAAGATAAGGATGGACT CTTTCACCTGAGTATTATC/T]AGGACACAATCGACGGGTGAATCTATTTGANTTATACCATAGGCC TATCTATATTGGGCCAAAGGGAAGGTAGGATGGGTACTGTGGAAACGGA

WI-21981	61 T A ---	---	TGTCATCTCATTTCTGGAGAAATCATAGATGTGGCAGAAATACATATTTCTTGAAGAAAAAAATTTA]GTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAAACATGCATGGGATAGA CACTCTGTTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGAGGCGTTTAAAGTTAAATTTGG
WI-21660	120 C T ---	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCCTCTCCACTGCT TACTGTGTGTACCAAGAGGAGAGAGAGCTACCCCAAGCCTAACCTGGCC[C/T]TGCTCTTTTTCAG GCTTCTCAGGATGCCACAGCACATACTGGGGAAGTGGGATGCAGGAGAGCCAGGGTCTGTCTTC AGAGGGGTACACAGC
WI-19105c	211 C T ---	---	TGGAAGTAGCCCTCTCGACAGAAAGAAATATTTGTGTCCATGTGGTTGAGTCTGTAAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTT GTCTGATGGTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCAGTGATCTCCCG ACAACTTC/T]CCAGGGGCAGGATTTCCACCCAGGGCCCGGGTGCCCG
WI-19105a	33 T C ---	---	TGGAAGTAGCCCTCTCGACAGAAAGAAATATTT/C]GTGGTCCATGTGGTTGAGTCTGTAAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTC CTGTCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCAGTGATCTC CCCACAACCTTCCTCCAGGGCAGGATTTCCACCCAGGGCCCGGGTGCCCG
WI-21760c	81 C A ---	---	CAACCTAGTCACTCTACTGATGCAATGATTTGGAGGTGCTCTCCTAGCTTTACAATAAGNGGAG GACCTCTGACTGCA[C/A]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAACCTAGTCACTCTACTGATGCAATGATTTGGAGGTGCTCTCCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATATTGTTCCAGCACCACTATTACTGTTATTATTTCTCTTTGAGGAAACCCAGGNATTAAAG AAATCTGTTTGAATTTCCATGATGCCCTAACTCTATGGTTAAAAATCCTTTTCCCTTACCAAAAAGGA ACTTCTTAATCACAGAGAAACAGAGGGGAAGACTGAGATATGTTGCAGAAAATTTATCTCTAC[T/C] AGAGACAATTCATAGTTCATAATCTTTCAGGGTTGCTTTACTTGGGGGC
WI-20934a	72 T G ---	---	CCAACATGCAACATAGTCTTCAATTTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA[T/G]CTAAGACAAATGGTCAAAATATTCAAATGGCCTGGCCTAGTGGTAATTCAGCAGAC AAACAGCATGAGAAAAGGCCGGGAGACAGTAATAATACGTGCCCATTTGCAATGAGTTACCCAATC AAGCCCTTTACCTCCTTAAGATGGCAGATTAGAAGACCTNTTCCCGAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATTCAGCCGGGCCATCAGAACAAATAGCATCTATACCTTCGAAACCTT/G]CCTCTTAAC CTCTCCAGGCAAGGAAAGGAAAGTATGATCATATTTGAATTCCTCAGAAATGGTGGGATCTCAAGACTT TTTAGAAAAGTGTCTTAATTAAGTATAAGAGGCTTGAATATAATGATGATAAATGGTAGCCTTTCTGGA AATAAATTTTGTGTAATCTGTTTAAAAAGATTTTGGGATGCATTGTCCCCA

WI-21961c	200 T G ---	---	---	AGCTTTGCTTGAAATTTGGTACTTACTACCTTGCAATCTCTTATTATTATTATTACTTTATTTTCCGTAAGTTATTGGGTACAGGAGTATTGGTTATATAAGTCTTTAGTGGCATTTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACTCGGCTTTATCCCTCGCCCCIT/GJC
WI-21961b	73 G A ---	---	---	TCCCACITTTCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTTATGC AGCTTTGCTTGAAATTTGGTACTTACTACCTTGCAATCTCTTATTATTATTATTACTTTATTTTCC[G/A]TAAGTTATTGGGTACAGGAGTATTGGTTATATAAGTCTTTAGTGGCATTTGTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACTCGGCTTTATCCCTCGCCCCCTC
WI-21956	26 T G ---	---	---	TCCCACITTTCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTTATGC CCCACTTGGGTCTCTTTCAAGTGAATTT/GTTCCTTTGTTCTTAAAGCCCTTTTAAATGAACTTCCATTCCCTGTTCTGAACCTTGCCCTAGTCTGTTTTCTGCTCATGCCCTCAGTCGAATCTTTCTTTCTGAGCGCGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGTTCGACGCCGTTAACTCAGGGTAACCTATCTCTTCCACCGGTAACAGAGGGTTACATTATGGGGTCCAGGTT
WI-21966	148 G A ---	---	---	CAACATACATTATGGTGCCTTTATTTAAGAAATGTTTACTGAGAATCTGTACTGTAAACAACATATTTTGTAGAAGCATGAGTGTGTGTGTGTGCGCGCGGCACGGCATGGCACTGAGG GGATTGCAATGGG[G/A]AACAGGATAAAAAGGTATAAAAACCTTGGTCCGAAATCTTTGCTTATTAACTTGGGCCCTGCTCCTCACAAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---	---	---	TATACTGGTTTTGGTTACATGGATGAATTGCTAATGGTGAAGTCTGAGATTTTAGTGTACCCATCACTGAGTAGTGTACATTGTACCCAACTGTAGGCTTTTATCCCTTACCCTACCTCCACCCCTCCCCATTTTGAGTCTT[G/C]CATAGTCCATTATATCACTCTGTATGCCCTTGCATACCCATAGCTTAACTCCC
WI-21139a	165 T C ---	---	---	GCTCTAGTGAAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGCTTGGTCAAGTCCCTGTTCTGCCACTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCCTTCTCTGTGAATGGGTACAA TGTGGGTACGACGTAAGGAACATAATACA[T/C]GTACAGCACTTCAGCACAAAGCCTGGGCACACAG
WI-20317b	217 G T ---	---	---	CACATGCAATGAAATACACAGGTAACTTTTAAACAGTGGGGACAAAATTTTAAAGTACGTGGCCAGCTGTTGGTTGCTTGTGGTCAATTAAAGACAAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGGTTACA AAATTTGTTCTCTTCAGTTTTTCATTAAAGTAAATCTAATAGATGATATACATATTACTGCAGATAAA ACCATCATCAGAA[G/T]TATTAAATTAATGCATATTTTGGGCTACTCT
WI-22082e	179 G A ---	---	---	CAGGACITGGTTTGTGTCCTCAACTGCACATAAATGTCCTTTTGTGTTGAGTTATTGGTTGTGCGGTTTTCTTTTGCATAAGAAATATGTCCATTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGGAGG GTACACGGGGCGTCCGCTCAGTTCGCCGCGAAGGACGATTC[G/A]CTGAACTGGGACGAGTCTACTCTC CTCCCCACAGGAGCCACGATTTCAAATCCTCTTTGCTGCAACCTCT

WI-22082b	67 C T ---	---	---	CAGGACTTGGTTTGCTGCCAACTGCACATAAAATGTCCTTTTGTGTTGAGTTATTTGGTTGTGTC /TGTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTTGTCTTATCCGGATGACGG AGGTACACGGGGCTCGCTCAGTCCCGCGAAGACGTATTCGCTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTCAAATCCTCTTTGTGCAACCTCT
WI-20993	139 A G ---	---	---	AACACAACTCCATGCTTTCAAGATCCCACACCCAGACTACTAAGACATATTAAAAATTTACAGCAAT TAAACAGTGTAGTTTGGTACATAACACATATAGCAATGATACAAATAGGGGAAAAAACCCCTGG GCTTCTT/GJTAACAAGTGTAGTATACATTAAAGACAGTATTGCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTCAAGGTCTTCCTAGCTCATCCACACATCACC
WI-21723b	125 A G ---	---	---	AAGCGATTTTATTAAATTTGATTTGGACATACTGTAGGTCAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G/A]ACATAAAATTTAGTACTTCAAAGGGTTAGTCATATTTCCCA[G/A]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-21723a	82 G A ---	---	---	AAGCGATTTTATTAAATTTGATTTGGACATACTGTAGGTCAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G/A]ACATAAAATTTAGTACTTCAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-22132	99 T G ---	---	---	CAACAGATGCTTGAGCCAAAAAAGCAACATAGGCAGAAATACAAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTGCTTTTACTATCCTTTT/GJCCCCATTTCTTCTAATCTCTTTGCTTTACAA TATATTACCTTCTAGGTATCACCTCATCTATAGGAATGCCCTCTAGTTTAAATGTCTGCCCCAAACA ATACTAACCCATTGAAGGATAACTATGGAACCTTTTAAATGGACAGTGGG
WI-21006a	106 A G ---	---	---	TGACAGATCACACCACATTTTGTGTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAAGCCAGAA GATTCCTTAAAGAACACATACACACATGTGCACACAC[G/A]GAGAGGCAAGTACAAAATGTAACC CCACCAAGTGCATGTGAATGAAAGTGCAAAAAAGGCTTCATTTGCAGAACTCTGAGGATCATTCTCT CTGCTTCAGGAAATAAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138 C G ---	---	---	CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGCTTGGAAATAACTGAAAAGATTTCAT TTTCTCTTTGTGTACAAAGGATTCAAATAATTTTACATCTTCTCTGCGCAGTTAAACGTGCCGTGG CTC[G/C]AATACACACCAAGCCCAAGCGTAACCTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166 G A ---	---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTCCATGCATGCAACTGTGTGGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAGCTGTGTGCTCACTTGTTCATATAA CTCAGGCCACCCCTGAAATATCTGTAGTGGG[G/A]AATTTACAAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAAATAGGCATGGGCAAT

WI-21079a	50 G A ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTGCCATGCATGCAACTGTG[G/A]CGCAAAATCAAGT TGTTTTAATACCAGTGTGCAGCTTGATTCCTCCATGAATTAAGCTGTGTGCTCACTTGTTTACA TAACAGGCCACCCGAAATATCTGCTAGTGGGAAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45 T G ---	---	TCTGTAGATTTAGCCATGCCATATATTAACITTTAAGGAAAAGT[G]GTTATATAACAGTCATTGCT TGGTAGAATCCAGTGTGCAATAAGTTAGCTCTAACAGTTAAACATTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAAATATAAATAATTTGGTGCAAATCCAGNAAAGGGCA TTAACCAACATGGGACTGATCTCTGGGGCTTCCACCTGACTAAGGTTTTA
WI-21941	79 A G ---	---	TGGAGTTAAGTGGGGCTGCTATTTCCCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGCAGAC/A/GJGGATGAGGCTCTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGGAGCCTCACCCAGAGAGCCTCACTGCATTGACCCACACCCACTCAOC CAGCACACAGGCACACGCGAGGGGCACACGACACACGNTGCACTCACCCACGC
WI-18916b	42 C T ---	---	AATGGCATCCCTGTCGATACCAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACITCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACCTGGACACAGCCTCAOC AATGCCACCTTCATA
WI-18916a	35 G C ---	---	AATGGCATCCCTGTCGATACCAACATCTTCAGCAGCTCAGC[C/T]GAGCCGGCTTCCCACITCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACCTGGACACAGCCTCAOC AATGCCACCTTCATA
WI-19828c	200 A G ---	---	TTCCCTTCTCCCCAAGAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCCAGGCTTCTGGCCCCAATTTCTGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCCTCTGACCCCTCACCACCCCAAAAT[A/G ]CTTTTAACTCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 C T ---	---	CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTGCCCT[C/T]AGCTGCATGCCACCCTC ATATCCACCCCATCCAGCCTCCTGCCCCGACACCCCGAGCTCCCTGCTCTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCCTTGATCCAAACACAGCATCT
WI-19860	51 C G ---	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C/G]CTGCATCAGTAT CTCCCATCCACATAATTTCTGTTGATTTTGCCATTACCCATAAAATGTTGGGATCTACCTCCCT CCTTGCAAAATTTGAGCTGNNCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-19889b	80 C T ---	---	ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGGG[C/T]TACAGCAATTTATTTCCCTCTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCTTGGCCACAGTCGTAACATTGC



WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTGCTTCTGGAACATATTGGAACACTTGTTTTCATAAGCTGTCTGACAGT GGCACAAATCCCATCCATCTTCAGGCCTTTTAAAGGTCATTATGAAATCTGAATTTCTAGJTAAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAACTCCTTGCCGGTGACGCTCTCGG AGAACATCTAATATTGAGTCTAGTTCTGTGCGGAACCTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAGGATGAAATTCACATTTATTTTNCCTTTATGTGAATAGAAATGGCAGTGAAGTGTCTCTATG AACTGAGGGGAGGAATGGCATGGCGTGGCGTACCAGCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGAGGCATCATAGAAAAACCCCTCAGCCAGAAGTTAGGACATTGTGATTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCTCTGCAGGCTCTGGTTGT/CJTTCATTTGCAAAATAAACCCA GACCGGGTCATCTTCAGTCCCTCCAGCTCTATTTTATGATTGCTCTTAGTCTTTATGAGCCA TGATGATTATCAGTCTCCCTGATGCACTCACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	---	GACGTATCTCTGAGGGCTCTGCCAGGTGATTAGGTGAAGAGGTTTATGGGCCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCATGGGTGAGTGGGATCTGGGGGGTGCAGACCTTGCTTTT /C/TTTCCAACTCTCTCTTAGCCAGAACTTTGCGAGAGCCCTTTNATTTCTCTTCCCTCTATTCC CCTCCTTTCCCAATGTGCTAAGGTCCCAATTCAGAGCCCTCCAG
WI-22292	53 A G ---	---	---	CCAGTGAAGGGTTACAGCCATAGTGAGGTCCCCATTTGCTCAGTACCAGA/GJGTTTGAGTAC GGTGCTTAAAAATACTTATCTGACCACAGTGGAAA
WI-22387	186 C T ---	---	---	ACCTGCACACCTGCCATCCGGTGCCATCTCCTGGTGGCACATCTATCCCACTCTGGCTCTGAAAG GCTTGTCAACCAAAATGGGAGCTGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGACCCCTT TCACTTGGGTCTAGCATCCAGCTCTCTCAGCAAAAGGAGGATTGGT/C/CTTGTGTTTCTG AACAGGGCCCAAGGCGAGCCAGGCATGCCATCACTGCAGCACTCAACCCCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAATTAAAGTCAAGATAAAGGGGCACTCTTTAAT/GJAAG GAAATGTTACCAATCCATAGTGAAGAGTGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCCTGAGTGCCCTCACCCAGCTACACTTACCTTGTATCTATAAAGTGTAAATTTAGAGT AAATACATTTGGCTGTAAAGTCG/CJGATCAGGTGCTCTCCACCAAAAGCAAACTGCTGA AATGTGGCAAGGTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTCGACAGTTTGTCTTATGTTCAGACAATCAAGNCTGCCCTTCAGGCACAGCCAGTGCCT /CJCTGGATGGCATCAGCACAGGCTCCCTGCCCGGCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59 T C ---	---	---	ATTTTCCCTTCTGTGTTTGTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGA/TCTGGAA ATCTGCATGATTAAATAACATTAAAGTTCATAACACACCCCATATCAGAGTATAAGCAAGAG GTTGAAAAATATCCCTAACCGAATGCAAAATAGGTATCCCTCAAAATTGACATTCTCCTCCTAGTT T



WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTAAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGCCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTAG/CAGACATTGCCTGTGCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTAAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGCCTCAGACTGTTCTCAGTCACT T/C/GCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTTGAGTCCCAGTCGAGGGTGCATCTTCCCTTTATCTTGCTTAAGCCACTTGGGTA/AC/] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTGAGAAGTCCCTGGAGGGAGGAGGCTTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC TTCCTTTT/C/GAAAAAATACACAATGGGAACGTGACA
WI-21965a	112 A G ---	---	CAGGTTCCACCAGAGGCTTTATTTCAGCCACTCAGGACCCCTTCTGCTCCAAGGCACTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGGACCTCCCCACAGCC/AG/CCCCACAGGGTCTCTGTT TCCAAAGTCTGATGGAATCAGGCAAGACCTTACACATTCACCCACTACCTGCTGGAGAGGGGTC ATGAGGCAGCCTGTGGTGGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAATTAACCCAGATGGGTGTACATTTTNTTCAAGTTCA AACCACATGGTTCCCTAGTCAGAAAGTCTCATGGACTTCTCCTAAG/C/GTGTCTATGATCAGAC CACCTCCTAAATGTGGCTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAGAAATTTACAACATTGACTATACAGAG TCTTCAATCCAAAACAGTTAATAGTAACCTGGTGGCACATACAAATGCATTGAATACTCTGTAT TATTCAGTAACATAAT/C/JAGGNTCCTGCATCATCTCTTTCACA
WI-22250b	132 C T ---	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAC/TG/ATAGTGGGTATTATGGGGTCTCTGCCTCCTGGCTGTGTTATGC GGANCCAGGAGTGGAGGAGGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAACTAGAAATCCTTGAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAC/TG/ATAGTGGGTATTATGGGGTCTCTGCCTCCTGGCTGTGTTATGC GGANCCAGGAGTGGAGGAGGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCCTCTCTCCAACCTCCAGGCCACCTGGGGCCAGAGCACCTCATGCCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCGCAGGTTCTCGGCTCTCAGGACGTCACGAAAGTGGA GCCAGAGGTTTGTGGGACTCCAGCCAGGGGATGAGGCCAGCCCGCCAGAACCTG/C/JAGTGCTTC TTTGACGGGGGCGCGTGTGCTCAGCTGCTCCTGGAGGTGAGGAAGGAGGT





EST22917 6	74 C T ---	---	---	GTAAACCTTGCACGCGCATGCTAAATGGAAGCCTGACTGACCAAGGGCTCTGGGCTCTCAATGCA ATAGAAAC[CT]TGACATGGGGCCAAAGACTTCCAGACAAAGCACGCGAAGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGAATTAACCCCTCAGGCTGTCTACTCA[ GTGTGGTTTGTAGCCTCACTCGACACAGGAAGCTTGAATTTGGAGGCTCCAAAGTCACTCTCCA GAGGGGAACTTCAAGAGGATTCCAACAGTGAAGCAGATCATGGGGCAAAAGTC[AG]CTATGG GGCAGACTGAGGTTGGACCAACACAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCAGGAGTAGCCAT
EST36745 3	56 A G ---	---	---	TGTGACCATACCAACCTATGCAATAAAGAAAAAATCCTCATTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATAACAAATGTGTATCTCCTGAGACACATTTATAACATTTCTGGTATG T[AT]TATTGTGAGTGGTCTCTAGTGGCCAAAT
STS- R37410c	201 A T ---	---	---	TGTGACCATACCAACCTATGCAATAAAGAAAAAATCCTCATTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATAACAAATGTGTATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAAT
STS- R37410b	139 G T ---	---	---	TGTGACCATACCAACCTATGCAATAAAGAAAAAATCCTCATTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAGTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATAACAAATGTGTATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAAT
STS- R37410a	48 C T ---	---	---	TATCGTGGGAAGTTCCAACTCATCTATGCTGCTTTTCTACTTGCTAATTTGGATGCTTCTTGCCA GGCTC[CT]TAAATTGTGCTGTAACCTGGGAAGAAACCTTCTACTCTCCACAACCCCTGAA CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGGTTTCTCCCGGGATGGTGAAATGTTCCGGACCTAGATA[CT]GTGACGA AGGTAGCAGCAGTGTGAGTGCACTAA
UTR- 04350	125 C G ---	---	---	GAAATAAACTAAACTGCAAGCAATCACTGTAAATAAGAAATGTTCTCTGTTT[CT]GACAGTTG AAGTGGGTGTGAGATGGCATAGCAATGAACAGTGGGAGCCCAATGAGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAATGTAT
stSG1026 6	55 T C ---	---	---	GTATAATTCAGCATAGCCAAAGCCTTTAAATAACCAATACATATTTTATGAAATCTTTTACA AGAT[GT]AAGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1028 2	70 T G ---	---	---	CACTTTAGATATGAGGAAATGGTTTTAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGATATGCAATAACAGCAATAATTTTTTCACT[CT]ATG TCAATGCCAATGCATTGAAAGGCCCGAGAAATGAGAAAGGATAACAACTTTTGATAAAAAAGGTA AGAAATTTCTGTGTG
stSG1031 0	128 C A ---	---	---	

stSG1033	116	T C ---	---	TTTAAAGCTACATGCTGAAAGAAATGATGCTGCTGCTGATGAAATAAAGGAAGAAAGGATGCATTTCCGG GCTCCAACTGCTCCTAGGAAGGCCTAGACCTCAAAACACCAACCACTCCAT[C]GCAATTTCCCTCTTTGG CTACTATGCTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTCTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1033	107	A T ---	---	TTTAAAGCTACATGCTGAAAGAAATGATGCTGCTGCTGATGAAATAAAGGAAGAAAGGATGCATTTCCGG GCTCCAACTGCTCCTAGGAAGGCCTAGACCTCAAAACCA[A]TCACCTCCATGCATTTCCCTCTTTGG CTACTATGCTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTCTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1243	225	G A ---	---	ATTGGCAAATGGGAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAAATCCTCCTCTTG AAATTATGTTCAAGCCAGCATGGTAGCTTATGCTGCAATCCCAGCACTTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTCGACACCAAGCCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATTCGTTTC[G/A]AAAGTATTTTCAGACCAAAAGGAGGT
stSG1345	60	G A ---	---	AACGTACGTATCACAGGGCAAGTATCTCTGTCATAAAATTTGAACATGTTGCTTCTTAC[G/A]CGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCATAAATGGGGCAA
stSG1345	54	T G ---	---	AACGTACGTATCACAGGGCAAGTATCTCTGTCATAAAATTTGAACATGTTGCTTTCGTTACGCGCT TCACATTTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCATAAATGGGGCAA
stSG1385	117	T G ---	---	TTAATGTCATCCAGGGAGGGGCCAGGGATGAGGGAGGGTTGAGGAGCGAGAGCGAGTATTTT TGGGTGGGATTCACCACATTTCCCATGAAGAGGGGAGACTGGTATTTTG[T/G]TCAATCATTAAGAA GACAAAGGGTTTGTGAACTTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGAGCTTCAGTCCCTTCTCGTGG
stSG139	69	T C ---	---	TCGTCTCCTTTCCAGTGTCTTGCCAGAAAGCATCCCCATGATGTTGACCGCACAGCACTTTGTGTCT TTCGCTTTGAGCACTTGCCACTCTGGCTGGTGTGCTGCTGCCACTGATTTGTGTACTGTCTGTGCTGCC GATCTGTTTCAGACAAGGCTGATTCAGAGACTCCACGTGTTCAAGGCTCTGTTGTTGTCATCCCT TGGCTCCTCCACTTCAGTTTGGCTTCTGCTCCTCA[T/C]AGTCTCTCTCCATGTGGCAACAAGATGGC TACTGTGTGTCACAGGTTACGTCTCTCAGCTTGGAAATCCAGCAGCAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1427	103	T C ---	---	CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTTAGGTCC[A/G]CTCCCTTGCAATGA AATGTGGGAGAGGGAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTTCCCTATCCTACC GCA
stSG1471	50	A G ---	---	CAAAACCAAAATCCTCCACGATATATTACTATTTAGTCTAAGT[C]TTTAATTCAAAGGTTGAGA ATGACGAATTCAGAAATTTCTTTCATACATAAATTCCTTTCCTTAGTTCTGCAGATGGGTA
stSG1483	44	T C ---	---	CACACCCACAAGTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCAAGTGTGCA [C/G]AATGTGGAGGATGTCTGTTGCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAAAGGAA AATGCCTGA
stSG1696	67	C G ---	---	

stSG1847 b	95 G A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAGAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATGACTGTGCT TCAACACAACTG
stSG1847 a	49 C A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTAC[C/A]CTAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATGACTGTGCTG TTCAACACAACCTG
stSG1897 a	83 A G ---	---	CTTAATGCCCTTCTCTCTTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGACACAGGACTA/GIGCCACACCACCTTCTCTCCCGTCTCCCAAGATGACT
stSG2022 a	86 T C ---	---	TGCTTGAGGTTTCAAACTGAGATATCTATGGCAAGTTTATAAAAGTACATTGATCAAGGTACAA TTTTAACATTAAATATACAT/CJATTCCTAATCTCATCTATTTAACATTAAACACAGGCCTTTGTGT TGTTATTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGCCTCAGTTGGGGGTTGAC T
stSG2076 a	104 C G ---	---	AAACGTTGTCCCAAAATGTGTTTCAGTTTCAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAATATATTTTGACATT[C/G]ACATCAGTGGGGCATTTT
stSG2108 c	71 A G ---	---	TTGAGCAACAATGATTTCGGAATGGCAGCTCCAAACCACAAATGATTGAGGGCTCCACAGAGA GAGC[G/T]AAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGCTTTGATTG GTTACAGTTACACAGTTGCTTATTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---	---	TTGAGCAACAATGATTTCGGAATGGCAGCTCCAAACCACAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGCTTTGATTG GTTACAGTTACACAGTTGCTTATTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAATAATCTCAGATGGCAGCACCCTGCGATGGCGATGGTGAGGTGGGT GCAGTCCCTGTGGTCTATTGCTTGAAGAGAGAAAG[G/A]GAGTTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTTGCTCTG
stSG2141 a	113 C T ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTGAATAATCTCAGATGGCAGCACCCTGCG[G/C]TATGGCGATGGTGCAAGGTG GGTGAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTTGCTCTG

stSG2148	50	A G ---	---	TGGAAACAACCGGCTATAGTCTGAGTCATATTTTAGACCGTGATTTTC[A/G]AAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68	C T ---	---	CTCAATGAGGACTCCATCAGCCAAAGCGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGCT [C/T]GCCGGTGAAGCTAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT AAGTGGCAGAGGGAAGGAGTGAAGGACCA
stSG2189	41	C T ---	---	CAAGTGGTGAAGCTGGGATTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACTCATCGCTAACTTTTGAGCACTTAGTGTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTCGAAC
stSG2200	49	T C ---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGGTCTGTATGATG[T/C]TTTATATTTATGTAT AATGTCTTACCTGATGATACCCCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85	G T ---	---	CATTTCTGCCTCCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAAAG[G/T]AGAGCATCTCCTCAGCCCTGGAGACAGTGTGGAGCTTCAGCT
stSG2257	65	A C ---	---	TCAGTATTGTAGGAGCTGGTAAGTCATGTCATAAAGTCTGTGAGGCAAGGCTATCAGAAGGGCAG[A/ C]GTGCAGGAAGCTCGCCAAAGCACTGGGCTGCTGCTCAGGCAGAAATTTCTTCCT
stSG2306	67	A G ---	---	GTCATCAGCGTAGAGGTCACTGGTATAACAACAGTAGCTATATGATATTTGGGAACATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAACTGATACAACCATGAGGTGAACACTTTTCACTGTTTCACAG TTCTCCAGAGA
stSG2334	70	T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAGAGAGATGAAAGAAAAATCCCCGCAAAAAACA AAAAAT[G/T]GCAGTGGAGGGGCTGTGGAGGGGTGAATG
stSG2339	63	T C ---	---	AGAGAGAAATGGTGAATCAACAAGACCTCAAATTTGCTTGACTGCAGAAAGTAACTGCTGCAC[T/C] GTTCTCAGAGTCACCATACGGTGACTGTGCTATTTCTGGCTGTGCTTCTTATTCATCA
stSG2465	76	C T ---	---	CAAGACTAAGAAAGCCGACCCGAGTGGTCCCACTCAAAAAAGAGATTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140	T C ---	---	TTGCAGGCTTGTATTCACAATAACAAGTCATGTATAGAGAAATGTGAAATGATACTTGAAAAACCAA GATATATAAATATTGAAGTCATTTATGCCCTTTTGTGACTGGTTAAATATGCAAAGCAGCTAAAG GAATAT[T/C]TACACCAACCCACCCCTTTTAACT
stSG2577	123	T G ---	---	AATTGCCAAATGGAAATTTCCAGAGGATTTTAGACCAACTTTGCCCTGTGCAATCCCAGTTTGGT CCCAATATAGGCCTTCTGCAAGAGAGATCAATGCCGAACCGAACTGTGAAGCA[T/G]GAACAATC CCGGCCAGATTAAATTAT
b				

stSG2577	121	C T	---			AATTGCCAAATGGAAATTTCCAGAGGATTTTAGACCAACTTTGCCCTGTTCATCCCGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAG[C/T]ATGAACAATC CCGGCCAGATTAATTAT
a						
stSG2700	58	G A	---			ATCTCTCGACTGCTTTAGTGGGAAAGGAATCAATTATTTATGAAGTCTCGGGCCCG[C/A]AGTCAC TCAGGTTTGGGAAATAAACCACTGGTCCAGAGCAGAGGCTACTTTGAGCCGGACACCA
stSG2724	101	T G	---			AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTCTTTATATTAATATTTGCAATGCTATAAT TTAATACTTATATTCCAATGCTTGCAATATCAT/GTTTTTTTAACTCTGGGGTGTGAAGAAC
b						
stSG2776	65	G A	---			GTGGCCGATCTTTACTTTCCAGAAAGGCGGTAAATAAACCTGTAGAAAGTCTCGAATATGC[G/ A]ATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAACCCACAAAA ATATCCACTAATCCCGAATATAGTAACCCCTGCTTGTCCGAATG
a						
stSG2791	109	G T	---			AAGGAAAGGTGGAGGGAAGGAAGAAATACAATGGTTAGAAAGAGCAACTAAAGATTATTC TATTACTTCTGAACGGTAACTAGCAATTTTAAATAATTT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
b						
stSG2791	100	A G	---			AAGGAAAGGTGGAGGGAAGGAAGAAATACAATGGTTAGAAAGAGCAACTAAAGATTATTC TATTACTTCTGAACGGTAACTAGCAATTTTAAATAATTT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
a						
stSG2826	85	C T	---			CCGCAATTTCAACACACATCTATGAAACTAAGGGTGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACAAC[C/T]GAACAAAAATAAGAAAAACCCATGAATGCCAGGTTTA ATTTTTTTC
stSG2850	88	G A	---			ATGGGTGCATTGAAAAGGCAAAATTAATACTTTTCAGGCAGGGCTGGCAATTTAATGAGCTGA TGTGTCCTCAAGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCCCAT
stSG3031	71	T C	---			ATACTACGGGGCTGAAGGCAATGTGAAGAGTGACTGCAAGTCTCGCATTTTCTGTGGTGCAGC AAAT/C/GCCCTTTATTTAAATGATCCAGACATCTGGGCAGCATAGCT
stSG3058	81	G A	---			GTCCCAACTCTCTCTCTTTAGAGAAAAACTGTGATTACCTCAACTTGAATATGAACGTGTGATTG AAAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAGCCAAAAAGGCAAACTGGCTGAGGC
stSG3092	94	T G	---			CAGCATCTCCAGAACATTCCTAGAACTGAACCATCTTGTCATATTGAAAAACAAGCCCAAGTTC CAATCCAAAAATAAATGAACGTGC[T/G]GATAAACATTCTTATGGTTCCAGCCCCCTACTTT AGTT
stSG3230	95	A G	---			AAGAACTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCAGATACGAGCACCTG CATCTTTTAGTCAATTGTGAGTGAGTC[A/G]GTGGGGTGTCTAAGTGTCTGAACCTGAAGTAG
stSG3245	160	G C	---			ACATCTCATACCCAGTAAGATCAAGAAAGGAATATCTGAGAGCAAGCCCTGCTCCAGGGGCC CAGGTATGTGTAGAGGCCAGTGGGGGTGGCCACTTGGTGTTCACACCCCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGTT[G/C]GTACTTGGCTTAAGTACTCAIGCTTTAT





stSG3463	103 C T ---	---	---	GATACAGAAGATAGTGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTATG AAATAACAAATAATGCATACAGCTCAATGGGTAC[C]/TJGGAAACAAACTTGGCTTGAATAATTA CTGA
stSG3491 b	71 G A ---	---	---	CAAGATACTTCATTGTCTCTAAGTAGTGCAGTCTGGCAATAATTTCTCACGAACAAGGACGATTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAACTCTCTAATCTTTTACTGGCACCTGTGGATTCTATTAACTCATTACTATTTCTGTGATG ACAGAAATAAGTTAAC
stSG3523	33 C T ---	---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTT[A/C]/JGCATATATGTGTGTACAAACACACACACC CCTAATCTCCTCAAAATGCTCTTGGCATAAGTTTATCTCTTACTGGTCTC
stSG3536	213 A G ---	---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAATAATATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGTACAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGTGTAACGCATCTCAGTCTCTATTGTTTATTTGTTAAATGAGCTTG TGCACCATTA[G/A]GTCTGCTGGGTGTTCTCAGTCTTGGCCATGAAGTATG
stSG3583	112 G A ---	---	---	GAAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60 G C ---	---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAAATCAGGTGTGGTGT[G/C]JACG CCGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
stSG3589	101 T C ---	---	---	ATATAGTGTGGTAGCATTATAAATCCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAGT GTATATACCCCTGGCACAAAAACCCCAATGAT[C]/CCTATTTCCAAAGATGTATCCAGATGAAA GTATCCAAACAAAGCTATATACAC
stSG3590 a	70 A T ---	---	---	GAGAGATGAGCTATTTTACTTTTACTTAATGAAGATGTAAGAAATGATCTTCTTCTAAAAA AAA[A/T]TTTCTGTGATGCTCTTGACCTGTAGGAAACACATTCAGTTTCTACACT
stSG3619	78 A C ---	---	---	CAGTGAGACTTCTCATTTTATAGCAATAACATTTTGCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATT[C/A]AACAACTTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40 T C ---	---	---	ACATATGTAACCTGCCATTAGTAGCCATATTAGGATGAGA[T/C]JGGATTGAGAGGCGATGAACCAAGG ATGCGTAATAATCATTAATGAATAAAGTTATCTGGGGAACCGGCCATTTGTCCAAACATTTACTAA GTGCTACTA
stSG3646 c	70 G A ---	---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGATATATGATGATAACAATAATATGCTTACT GGT[G/A]ATTAACCTTTGATACCTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTTTTGA

stSG3646 b	55	A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATA/GJ/TATGTCTT ACTGGTGATATTAACITTTGATACITTTGTTAAGATGGTGTCTGCTAAATTTCTCCATTTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43	A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG/JTJGATAACAATAATATGTCTT ACTGGTGATATTAACITTTGATACITTTGTTAAGATGGTGTCTGCTAAATTTCTCCATTTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85	A C ---	---	ATTGTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCCTGGACTCACCT GAAATATCTACGAGGC/A/CJTCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAAAAGG
stSG3693 a	30	C T ---	---	ATTGTTCCCTGAACATTCCCGTGGTCTCC/CJTCTGAAAGCCGATGACCATCCAACCCCTGGACTCA CCTGAAATATCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAAAAGG
stSG3698 b	145	G A ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGACCCCAATCCCCAGGGTTGCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAAGTCT TTATTGGG/G/AJAGAAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51	C G ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGACCCCAATCCCCAGGGTTG/CJ/TCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAAATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107	C T ---	---	ACCAGCCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGCCATCCCTGGGCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG/C/JACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGT
stSG3725	104	G A ---	---	GCCAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATTACAGCCAAACAGCAACAGCCCG/G/AJAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAAATAACGGCACATTTA
stSG3751	128	G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGGATATGGTCCC/G/AJTT GCTGACTCCATGTGTGCAAGAG
stSG3787	49	T A ---	---	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTAT/AJAAAGTCCCTAAGA CACTGAGGGCATAAACCAACAAATAAATAAGGAGTATAGGCTAAAGCAGTATCTTCCCT
stSG3880 b	115	G C ---	---	GACAAGAGGGAAGAGATCGCCAGAGACAGGGCTGGGCGAGCTGGGGTCCCTGAGTCCAGGGCGC CACCACAGTCTGTGGGTCAAGGCCCTCCTCTGGGGAGCAGGTCTA/G/CJGGCACGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAAGGAGTCCATTTCTGCGCT

stSG3880 a	36	G C ---			GACAAAGGGAAGAGATGCGCCAGAGACCAGGGCTG[G/C]GGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGGAGCAGGTCTAGGGACGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGAGAGTCCATTCTGCCCT
stSG3895	44	A G ---			AATCAGCCATTGTACACATTGCAGCTATGATTTAGTGTGTA/GTJTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCAACTG AAAAAT
stSG3902	104	T C ---			TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCAGCTCTGGTGGAACTGGCTTCCTGATAACA TCATCTATTTACCTAAATGTGAACCTGCTTTCTTTTC[C/T]CAGCTCAATAGCTTAACATCTAATTC ATGTTTGTCTCCCTTTGCTGGACAAT
stSG3935	50	G A ---			GGGTGCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTC[G/A]CTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCAACAACCTTCCTGGACGT
stSG40	25	A G ---			GAGGAAGAGGTTGAAGAAGTGTGA/GA/AAATATATTTAAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGGTGTGATGGATCCCTTACTATTTAGAAATAGGAACAATAAACCCCTTGTGTATGTATCA CCCA
stSG4009	32	A G ---			GTGTGGGCTGTCTGATGATGAATGGCGCGCTC[G/A]GTACTTTTACGGCTTACACTTTTATGCTCCT ATGAATTTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGTTTCCCACACTGCTTACA
stSG4033	123	T C ---			AGAAGCCTTGGGGACAATGGCAGTGGCTTCTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTTT[C/T]GTGAAC AGTGGGCAACAC
stSG4038 a	29	G A ---			GCTGAGAGCACGTGTACAGCCAGCCTGT[G/A]CGCAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTACGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT
stSG406	53	T C ---			ACTGTGGTTCAACAGTATTGCGTTGTGACAGCTAGGAAGCTAAACGAACAAA[T/C]GGTTTTAGTT TTGCTGAAGACTGGCCTTATTAAATGGACAGCTTTCTCATAACAAGAGATTATTAACTTTTATCAGGTGT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55	G T ---			ATCTGGGCTGAATTAGTCAAGCAGGTGAGATACTATTGTCTGTAGATGTATTAG[G/T]ATAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27	A C ---			ATCTGGGCTGAATTAGTCAAGCAGGTG[C/A]GATACTATTGTCTGTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65	G A ---			TGCATGTTCCACATCTTTTCAACAGCAAAATGTATAATAAATTAACCTTACGTACTTATGGATAATCAC[G/ A]CTTTTCCCCTCAGAGAGGCCACAGTTAAACACGTTCCAGCACACCATTAATCCACCGAGCT

stSG4128	54 A G ---			CITGGCAGATAAGGGACTCGTTGCAGATATGACTTTCCTTTGTGTACATTTCTA/GTATATTATTT TACTTCTCTGAAATGCCACATAATTTGCAATAATGATTCACTCTTAGCTCCAAAGCAAGTCC TTTATCAAAATGCAAAATGTTCCAGAGGG
stSG4209 b	128 G A ---			CACGAAACAGATGACAGCTACACAGTCTGTAGGACCGAGGCTCAAAACATCCACATGGCACAAGC AGGCCCGGCACTCCAGGCAACGAAGCCACCCCGAACCTTGACAGGCGGCACTCCCTC/GA/GC AGGGGACCAACGAGGCGACAGGTGCTTTGATGCTCCGGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---			CACGAAACAGATGACAGCTACACAGTCTGTAGGACCGAGGCTCAAAACATCCACATGGCACAAGC /A/CAGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGACAGGCGGCACTCCCTCGGC AGGGGACCAACGAGGCGACAGGTGCTTTGATGCTCCGGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---			CATTACCCAGAACGCCATGGAGGACCAGAGC/GA/CACACGGCCGGGACTCCCGGATGGCTGGGGG GCTATGCTCTGACAAGAGATGACGAGGCGGCGGGGCTGCCTCCTCCCCCAGGGGCAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCCGGTCATG
stSG4301	81 T G ---			TGCAACAGCTCTGAGAGGAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACATTTCCAT TTAAGCAAAATAAATTT/GA/GCTTCTGAGTAGTTGTTCCAGTTTCAACCAACATTTTG
stSG4331 b	71 T G ---			CTCACAAGGCCCAACACAGAAAAGATACAAATACATTCACAGCTAATAATTTAGTTTATGACAC AGAGT/GTTTTCAACAAGTTTAAAGTGTACCTGAAGAGCATGTTAAAGATTAAAGTTATCACTT GGAGAGCAGATTTCTTGGCCTCGCCCTTGTGATTTCTGTTGAGGGGTGTC
stSG4340	76 G A ---			TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC/GA/TAAGTGGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---			TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCATCTTTTG/C/C/CCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4361 a	24 T C ---			TTCCCAACCATTTGAGTGACAGAGCT/C/C/AGTCATGCAGAACTCAGGTTGCATGACTCAAAATTAGG CACAAGTCTTGGAATTTCCATAAGGATAACTGCATCTTTTGCCACCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4376	73 A G ---			TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTGCAAGTGCTCTCCAAGGGGAG AACAG/G/CTGGAACCTCGGCTCTGCAAGAAGCCATTCTTCCAAAGCCATTCTCTCAGCTGC
stSG4381	50 T C ---			GAAGGCCACAAACACTCCATAGCCAGAGAAATGACAACATACGATTTTCTT/C/C/AGTCTTTAGT ATCCACAGTAGTGATGCTGTCCATGTACAAGTGTCTGCCAGAACACCCATTAAATTCATGCC ACCAATGGTTCTGCTATGTGATCCGATATTTTTGCCCGATCTGAATACTGCAAGGGCTTAACCAT TCAAAACACCGC/GA/GTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT
stSG4410	79 A G ---			

stSG443	65	C T	---			AGCAGATCAGTCAGCCCACTGCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430						TGTATGCAATGAGAAATACCAACTGGTAGGATGGGGAGGGGAGGAGGCAATAGGCAC
a	54	A G	---			AAATGGAATCTATCCTGGCTGCTCTCAGGTC
stSG4448	99	G A	---			ATGCACATTAAATGAATGGCTAACTACTGGAACTTTAGTAGTCTATAAGGT/A/G/JATTAAACATA
						GGTAGGATCCAGTTCTATGACAGGCTGCTGAAGAACAGATATAGGCATCAAGAGGGCCATTTT
						CCTCCCTCCCTCTCTTCCCTTCCAGTCTTTTCCATACTGTTCCCTCCCTCCCTCCCTCCCTCCCTCT
						CGCCTAGCCCTGCCCTCTGGGCTCACTGC/G/A/JTGGGTTAGGCCCTCCCAAAAA
stSG4449	92	T C	---			ATTAGCCATTCTTGCAACAATTGCTTTACTGTAACCTAAGAGTACTGTACTGATGATGTTTACAAT
						TAACTTTGGACAACCTTAAACTTA/T/C/JAGTGACATTGCTGTCTAATAATCAAATACTTTCATCATA
						GGCTGAACATAATTATTAAAGAGCAAAAGTTACCCCTCCC
						CAGACATGAGGGATGGCCCTGCTCTCTGGGACAGAGCCCTCA/C/JAGATGATGTCCATGTTTGTGT
stSG4467	42	C A	---			GAATGAAACTCAAAACACTCTTCAGTTTTAGAGTCAATTTCTGGTATCGAGCGACCACACCGAGGAG
						CACACCCTGCTTCCAAGGCTGCTGCTCTGTCACACAGT
stSG4475	21	A C	---			ACATGTCAATTCCTGACCAGG/A/C/JATTAAATAGTTTATTAGAAGAAATGAGTTGAAGTGAGCGA
						TTAAGAGACACAAACTGGACTTTTGTTTCTTTTACTGTAGCACCCAGGTTTCATG
						GTAACATTCTGGGGTGGGGTGAGACAAACA/A/G/JATGAACCAATAATTAATTACAATTATACATT
						TCAAGGAGACTTTTAACTAGTTAATGTGAACGACCCATCAATGGTTTGTGAGGAAAGGGGAGA
stSG4477	32	A G	---			TGAAGTCTGCTCTGGGCAACGTTTGGCCCTCATGCACTGACACTTGGC
						TGAAGTCTGCTCTGGGCAACGTTTGGCCCTCATGCACTGACACTTGGC
						TGAAGTCTGCTCTGGGCAACGTTTGGCCCTCATGCACTGACACTTGGC
						CAGCAGGCTGCTGCTGGGCAACGTTTGGCCCTCATGCACTGACACTTGGC
stSG4531	79	C T	---			GATTCTCATTTGACAGGGGAGACGCTGTTGTCATCAA
stSG4550	86	G A	---			TGCATTAAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATT
b						AAAAGAGACAGTGGGCACC/G/A/CAATTTGAGGGGAAGGGGGCAGGGTTTATAGAGAAC
stSG4550	85	C G	---			TGCATTAAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATT
a						AAAAGAGACAGTGGGCACC/G/G/CAATTTGAGGGGAAGGGGGCAGGGTTTATAGAGAAC
						AATCAGGCACAAGCTCGGGAGAGAGCCCAACAAAGCTCTTCTGCAC/A/G/JATGGGAGGGAGACAC
stSG4590	47	A G	---			CATTGAAAAGGCATGTTCTCTTCTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCCTTG
						AATCTGTATCACCCAGCGCTGGT/C/JCAATGTACTAGTAGCTTCCACAGGGATTTTATACTATTTC
						CTATAAGGTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTCACATTTATCT
stSG4623	22	T C	---			TAATATTCCTGTTCAAGATGCTCTGGAG
						TAAAAAACAACCCCCCAAAAAACACCCAGAGTTTTTATGTTTTTATGTTTTTATGTTTTTAAAG
						GTATTTCTTTCTTAGCTTCTAAATTTTGAAGTCAAT/C/JATCAGAAAGTCTCCCTACTCACAAGGTGA
stSG4843	102	A C	---			GAAAGGA

stSG4850 a	38 C T ---	---	---	GGAATCTAAACTGGGAATGGCCGAGGAGGAAAGGGGCTC/C/CTGTGCACTTTCAGGGCCACGTCAGGAG AGCCAGCGGTGCTGTCGGGAGGTTTCCAAAGGTCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGATTCTTGGGTCC
stSG4879	86 A G ---	---	---	AACTCTGAAGGGGTGACCTCAACCCAGCCCTTGTCTGTGAGGTCTGCTTTTGCAGAAATGCGCTG CCCTGGGACTGGAGCAG/A/G/CTTGGGTGAGCTCTAGGTGGAGGGTGGTGGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A ---	---	---	ACTGGACTGGCTGCTGCTGAGCCGGCTGAGCGGGCTGGGACTCGGGCTGACCACCTCGCTCTCAG AGACTGCCCGCGGTGACCACGACTACGCTCTGCC/G/A/GTGGGAAAGCAGAGCAGGACC
stSG4896	112 C T ---	---	---	AAACAAATCAAAACCAATCCCGAGCAGTCTATGTACAGGGCCACTCCCTGCTCTGCCATAGAGA GGTTGGGGGCGAGCTGAGGAGTGGTGGGGCTGGGCACCTTTCT/C/CTCAGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22 G A ---	---	---	ACAGTGCCGATGGTTACACAAATG/A/JTTGTAATGTATTAATCCCACTTACGAATGATTAATGA TAAATCTTATGTTTATTCATCACTACCAAAAGGCTGGGTGAGGGGTGCTGGTTTCTGGTCTT
stSG4950	24 A G ---	---	---	TCATGACTCCCGAGGAAAGGTCTT/G/CTTAGCTTCTCTCCCTACTTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAAGCATTTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ---	---	---	AGATACGGGCAAAACACTGGGATGGCTTCTCTGACAACTTAAGAGGTCTCCGAGTTATTTCTGGGT GGGAAACACTGACCCAGCCCTTATTCCTCAAGGACTTAGTCATTGGCAAGGAGGATTTCATGAGCC CC/G/A/GTGAACACAGATGGGGCCCTGCTCTATATTCAC
stSG4961	91 C T ---	---	---	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGTA/C/TJAGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ---	---	---	ACTGGTCCCTCTCAGCAGATTCAGGGGTGTCAGGGCTGGTTACCAAACTCAGTAGGAGTGCAA GGGCT/A/GJTACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTCCCTTTTCTTGTGTGC AACCTTG
stSG4997	22 T C ---	---	---	CAAAGGAGTAGGAGCCCAAT/C/JTTTAAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTAGAAGGGAGGAGGCAAGAA GGGATAGGGAGATGGTGATCCAAAT
stSG6312	37 C T ---	---	---	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAACAC/C/JTTATGCCATCGGGAAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107 G A ---	---	---	GCTCTGGTCAAGCAAAATTCAGGAGCAGAGCAAGCAAGGACAGTAACACACATGTATGACCCCTTA CAAGTGTCTTAAGATTTTAAAAATGTGATGTTTGTCCAC/G/A/JATAGTTGAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAACATTTTGTCTTTGGCCTGGTGTGGACAGAAAAGGTTGGCCAA ATGGATTGAGTGATGAGCAGCATG





stSG8145	97	CT	---	TTGTGGACTTCAAATTCCTTCTCAGATTTTAAATGACATTATGCATGTACATATTTTAAAAATTT AGACACATTTTAGAGAACACAATTGTGAAC[CT]ACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCCTCTGCTGTGAAGG
stSG8150	36	AG	---	ATTGTTCTTGCAATTGCTTGGATTTTTCAGAATAGT[G]ATATAAATAAATACGGGAATCCTAGGCAT TCGTGTTTTCTATGTTTTAACAGGATTTTCTCTAAATGTTTCGCTATTAAATACCATGCAGGAAATT GGGAAT
stSG8340	30	CT	---	AGAGGATTATGGAGAGAGCTGGGCAGGATC[CT]CAACATTATGACCCCTGAACCTCCAGAACTGGAT TCACTAGAAGGAGAGAGAGAAAAACGCTCATCAAAA
stSG8466	111	GA	---	TGTGTATTGGGTGACTGTAGCCTAAGGATAAATGAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACTTGGTTACAAGGTATTGCACTACCT[G/A]TGAAGCAGCACAGCAATTAT TTGAAAG
ESTD-ACE	--	--	---	GATCAAGCAGTGCACACGGGTACGATGGACCAGCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTCCCGTCTCCCTGGTGGGGGCCAACCCCGGCTTCCATGA GGCCATTGGGACGTGCTGGCGCTCTCGTCTCCACTCTGAACATCTGCACAAAATCGGCTGC
ESTD-ADA	--	--	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGTC CCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGTCAGTGTTCCTCTCCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAACTGGGACTGTGAGGACATGGAGCCCTCGGCACTGAGCTGCAGACCC GCAGACCAACTCCTGAGCTTCTGGGCCCTCTGAGTCTTGCTCTC
ESTD-AK-168	--	--	---	GGGAGTGACAGCTAGAGCACCAAGGGGGCTCTACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	---	AATCCCAGCACCTTTAGGAGGCTGAGGCAGGCATATCACCAGAGGTGAGGAGTTTGAGACCAGTCTGA CCAAATGGTGAACCCCATCTCTACTATAAATAACAAAATTAGCAGGCATGGTGTGCATGCCTGT AATCCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGGAGCGAAGTTGTGGTGAGCCGAGAT GGCACCAATTGCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGCTCTC
ESTD-ANT1	--	--	---	TCCTCTGTCAATTCCTACTCCATTAGTTCAAGGTGAGTGAAGAACTGGGGCAATTAAACCAAGTAATTCA TGGACTGCCCAACTCGGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	--	--	---	CCAGGTGTTGTGGCACGTGCCTGTAATCCAGCTACTCGGGAGACTGAGGCATGAGAAATCTTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCGCGCCACTGCACCTCAGCTGACAGAGCAAG ACTCC
ESTD-ARSR	--	--	---	GGAGAAATGGAGCCTGTGGGAAGGAGCGTCCGAGGGGTGGGCTTTGTGGCAAGCCCTTGTCTGA AGCAGAGGGGGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGTGCACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAACCATCAGTGAA GGAAGCCCATCCCCCAAGATTGAGCTGCTGCATAATATTGACCCCAAC

ESTD-AT3a	--	--	--	---	---	AGACCTCAGTTTCTCTCTGTAAGGGAAGTTTGTCTTGATCTCCATGGGCCCCAGCCAGCACTG GTGCCCTGTGAGTCTGATCAGGTAGAGGAGATGGGACAGGTGGAGGAAATTTGAAAGGGCATTTG GAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
ESTD-B3AR	--	--	--	---	---	GGCTGCCAGGGTTCCGTGGAGGCGGCCCTAGCCGGGGCCCTGCTGGCGCTGGCGGTCTGGCCACC GTGGGAGCAACCTGCTGTCATCGTGGCCATGCGCCGACTCCGAGACTCCAGACCATGACCAACGT GTTCTGACTTCGCTGGCCGACGCGACCTGGTGATGGGACTCCTGGTGTGCCCGCGGGGCCACCTTT GGCGC
ESTD-BA511	--	--	--	---	---	GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGTGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTGCCACTGCA
ESTD-BCL2	--	--	--	---	---	AGCTGATTATAACTCCTCTCTTCTCTGGGGCCGCTGGGGTGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTCTCTGGGAAGGATGGCGACGCTGGGAGAACAGGGTACGACAACCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTCCAGAGGGGCTACGAGTGGGATGCGGGAGATGTGG GGCGCGGCCCCGGGGGCGCCCCGCCACCGGGCATCTCTCTCCCA
ESTD-BCR	--	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTGAAACCCATAGAGCCCCGGAGACTCATCTGCGCAAGA GACCAAGAGGTGAGCTTCTGTGTCCCGGAAAGGAGGAGGAGGTGACAAAGCTAACTCTGCTTCAA ATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCTGCCACA
ESTD-BRCA1a	--	--	--	---	---	AAGAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACCTAGGGGAGGCAAAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	--	--	--	---	---	ACTAAATGTAGAAAAATCTGCTAGAGGAAACATTTGAGGAACATTCATGTCACTGAAAGAGAA ATGGGAAATGAGAACATCCAAAGTACAGTGAGCACAATTAGCCGTAAATACATTAGAGAAATGTT TTTAAAGAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	--	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTCTGAAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCCCTAATTTGCTCCGGGAAGCACATTCATCAA CCCAGTCAAGTTGGGGGACAGCCATGCACCTGAGCCCTCTGTGTAGCCTTCAACCATGCATTCATCTAA GCTCTGCAAAAT
ESTD-C6	--	--	--	---	---	

ESTD-C7	--	--	--	--	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	--	--	---	---	---	GGCAAGTTTATTGATAGAGAGGAATCAATAATGGCAATGAGGAGACATCACTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGTGACCCCAAGCAAGGAGGACCTAG TAACATAATTGCTTTCATTATGGTCTTTCCCGGCCTTCTCTCACACAC
ESTD-CB23	--	--	--	--	---	---	---	TAGAACATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGTCTTTCCGGCCTTCTCTCACACATACACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAAAAACGTTGCCACCCCGA GGTCGCTGTGTTGAGCCATCAGAAAGCAGAGATCTCCACACCCCAAAA
ESTD-CB24	--	--	--	--	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCCCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGCTGTGTTTGGCCATCAGAACGAGATCTCCACACACCCAAAAG GCCACACTGTATGCTGCGCACAGGCTTACCCCGACACGCTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGAGCAGACAGACCCGAGCCCTCAAGGAG
ESTD-CB25	--	--	--	--	---	---	---	GTTTCTTCAGACTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTTCTCTCTATCTTTGCGGTC TCTGCTCTCGAACCCAGGCTGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTCTGTCACAGAGTCTTACCAGCAAGGGTCTCTGTCTGCCAOC ATCCTCTATGAGATCTTGAGGAAAGGCCACCTTGATGCGGTG
ESTD-CB27	--	--	--	--	---	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGCCTGGTTGCATTTCAAGAGTGTCTGTGGAGTTTGTCTCATCATGACCTATCTCTGA TTAGGGAAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTTCTCTCCACCCCAATGCTGCT TTCCTCTGTTTCATCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD-COL2A1c	--	--	--	--	---	---	---	AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCCCTGTCACTTTCAGGGTGTTCAGGGTGGAAAAGGT GAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACATACTGCCTTTG GTCAGCCTATTGAGCTGTAATCACCATAACCGTACCT
ESTD-COL2A1d	--	--	--	--	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTCTGGGACCTGGAACTGACCTGACTTCTTCTACTGACGAGACAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATAATTTTATTGACCAACACTATCATGGAACAGC ATT
ESTD-CPT2	--	--	--	--	---	---	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGTATGCTTAGAA GGCAAAATCCATCAAAAGTTAACTTCTGGGAGATGAAAGCTACCATCACTTCTCATCATGAAAAC TGGGAGCGCGGCATAGTGTCTCATGCTGTAATCCAGCATTTTGAGAGGCTGAGGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTGGCCACAT

ESTD- CTLA-4	--	--	--	---	---	---	ATGGCTTGCCTTGGATTTCAGGGGACAAAGGCTCAGCTGAACCTGGCTACCAAGGACCTGGCCCTGCAC TCTCCTGTTTTTCTCTTTCATCCCTGCTCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCGAGGATCGCCAGCTTGTGTGAGTATGATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	---	CAGGCCAGCGTGGTCGAGGTGTCACCATCCCGCAGAGAACAGGTCAGCCACCACCTATGCACAGGT TCTCATCATGAAGCTGCTCTCAGGGTTCCCTTGGCCTGAGCAGGCGGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	---	AAAAACATTTTAAACACCTTTTCAATCATATACACCATAAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTCCAAATTAAGTCAATCTAAATGTCAATACTGATTAAATGCAAGTTCAACAGACA ACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTTATGCCCATAT CTGCAATGTC
ESTD- D17S33	--	--	--	---	---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCAATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCGGTG GGGTTGTGGCTATGTGTGGTCTTGTGTAGACGGGGCTTGGTTTCAGTTGCACTATTGCGTTATT GCAGATTGCTTTGTCTTCCACTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	---	TTTGAGACCACCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATTAACAAATAGCTGGGTGT GGGTGATACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGGCAGGAGAAATGCTTGAACCCA GGAGGCAGAGCTTGAGTGAGCCAAAGATCACACCCTGCACTTACAGCCTGGGTGACACAGTGGAGA CTCTGCTCAA
ESTD- D3S11	--	--	--	---	---	---	AACTGATTAGAACCTGAAATACATATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAGTACACTGTAATAAGAAATTAACAGAAATATCATTTGT TTATTCAAACTATTTATCATCTTATTTATGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	---	AGGTTCCACATTATTGCTGATTTTCTGATGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTAATTCAAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGTC TGAGTCTTATCAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAAGTGAACATACTGCTCTAGAACCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTATTTTGGAAAGGATGCCGATGT
ESTD- D4S338	--	--	--	---	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGCGAGGTATGAAATGTATTT CTTAAACAATAAAGTTGAAAGTCCAAAATTTACTCCTTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCAATATGTTTCATCAGAGCCCTTGGGTGACCAAGGTGATT GCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTTTCAATGCAAGTAG
ESTD- D4S95	--	--	--	---	---	---	CTTTCATGACGATAGGCTTCTCTACTAATCACAGAAATTTTGAGAGAGCAAAAACAACTTTCAAGG ATAATGGGCAATCACTTCTTCTTCTTTAGAGTCTACCGG

ESTD- D7S399	--	--	--	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTTTTACAAACATTTTCCATGGACTCCATCTAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	--	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGGCTCAAGCAGCTGCTGGCCTCCACT TCCATGGGTGTGGGGCTGGAGCTCACTGTCCCTGGGAGAGGAGGGAGTGGGGAGGGAGACA GAATGCTGATTATCTGGTGAGAACCAAACTTCTGGCTGTGGTGGGAGGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGGAAGAGAACAGAGT
ESTD- DRD1	--	--	--	---	---	TCCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAAGATCCAAACCCATCAC ACAAAACGGTCAGCACCCCAACCTGAACCTCGCAGATGAATCTGCCACACATGCTCATCCCCAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	--	--	--	---	---	TCTGGCTTTGGTGACGAGGCTGCCGGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCGGTACAGCCCCATCCACCCAGCCACACAGCTGACTCTCCCGACCCG TCCACACGGTCTCCACAGCACTCCGACAGCCCCGCAACCCAGAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	--	---	---	AAGACGATGGCCAGGATGAGCGCAGTAGGAGAGGCGCATAGTAGGCTGTTGGGGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCCAAGGTGTAGTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGCGTATGCCAAGGGGCTTCTGTGAGGAGA
ESTD- ERB82	--	--	--	---	---	TCTTTCAGGATCCGCATCTCGCCTGGTTGGGCATCGCTCCGCTAGGTGTACGCGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCACTGCGGGGCGCGGTGAGACCCACCGCGGCTGGAGGACTTCAACC CGCCTCACCTCCGTTTCTCGCAGCAGTCTCCGCATCGTGTACT
ESTD- ETS2	--	--	--	---	---	ACTCACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGCAACAGGAAGCCGTCCTGGCGCTGGCA GTCCGTGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTCTGGACACACAC AGACTATTTTAGATTTCTTTTGCCTTTTGCACCAAGCAACAGCAAAATGCAAAAACCTTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCTTTCAGAAAGTTAGTTG
ESTD-F2	--	--	--	---	---	GATAAGTACACTGAGGGCCCCAGGAGGTATTGCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCCCTCCAGGCCCGTAGGGGAACCTGGGGGATCTAGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGCGGTGCTGGGTCCCAACAGAGGAGGCCGCTGGAGGAGGAGAGGATGGGC TGGATGAG
ESTD-F9	--	--	--	---	---	AGATCCTGATGATTTTTTCTATTTTTTCTAAATGTTTTACAGTTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTTGTAGTTAATTTGTGTAAAGTATGATGTTTAACTCAACTTCAATTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC

ESTD- GODH	--	--	--	---	---	CGCAGACCGGTGAGTGTGGGTGGGAGTGTGGAGGGAAGGAGGAGGAACCTGGGGGTTTAGGGACT TTCCGGGTGACTTCCCGTTCTGTGCTTGCAGAGAAAGGGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGAGCTCTGTGTCGACCGTGTGTCTGCTGCCCTGTTACGCTGTCTGTGCGCGCAGTCGA CTCTGTCCCGGAAATCCGAGAGCT
ESTD-GCK	--	--	--	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTACGCCCTGCTGAGGCCACTCCTGGTCAACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGATCCOCCACCCACACCTGGCTGG AGCAGGAAATGCCGAGCGGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCCAGGTCACAG
ESTD- GNAT2	--	--	--	---	---	GACCCTGAGTACCTOCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACACACAGGCATCATTTG AAACCAAGTTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCTTAGG
ESTD- GPPK2L	--	--	--	---	---	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTACCGCGCGAGAACTGCTCGATATC
ESTD- HPRAS	--	--	--	---	---	CTGGGCTCGCCGCGCAGCAGCTGCTGGCACTGTGACGCGCGGCCAGGCTCAOCTCTATAGTGGGTGCG TATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	TTGGAAGTTTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCTGGGCCCCACATTCTGGCCTTG AGGGCCTGCAGGACCCCAAGAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTACCAAAGCTATGATAACCTTAATTACCCCTGAGCAAGAGTTCGGCCTCCGGCTTGATTCC AGATGGAGCTTTCCTTATCCCTGATGATGGATTGGCTTCCTGCTG
ESTD-HT2	--	--	--	---	---	GGGCTAAAAATTTCCGAGCAACTTTCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTGAGAGAGATAAAAGGATAACCTGGGGTTTTCTGTGC TTTGCTTCTTCACATCCCTGGGGAGTTAATAGCTGCAATTTTCAAAGAACGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTCAAACAAGACACACCTT
ESTD-HT4	--	--	--	---	---	ACCAACGAGCCGGGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGTGCTTCTATCGGCAAGATGCGTACTTATTTGAATAGTAGAGGTAA ACACACGCCCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	AACACACAAGCCCCAGCGAGAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTGGTTTTCTTCTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTAGCTTGAGTAAATTCAGGATATTCTCCTACAAAATGAAA ACATTTTCGTCTGTAAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	--	---	---	ACCCAGTGGAGCCCGCTCATTTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAGAAGGAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	--	---	---	TTTACTATTCAATGGATACAGAAATTGTGGGAGTCACTATATCTCTATGAACAAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATGTTGAGTGACGGGAGTGGTGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGATACGAACGAAAGT ATGTAAATACTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	---	---	CAAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATATTATTATTATTATTTTATTTTGG AGATGGAGTCTGGCTCTGTCACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCCTGGGTTTCATGCCATTCTCCTGCTCAGCCTCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	--	--	--	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTCCTGCTCAGGAGCTCTCTGTCATTTGCAGG
ESTD- KRT10	--	--	--	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAAATGCAATTTAAAGTAAGTAACTGCTAAGGTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCAAGTATTGATA
ESTD- KRT8	--	--	--	---	---	ACCCTACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCTCAAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCACGTCACATTTGACACA
ESTD- LF79	--	--	--	---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTGAACCGTAGCAAAACTGCATTGGTATTAGA AAATAAAAATTTCCAATATGTAGTGTGTGTATACCTGCTGCTGCATGCAGCATCATAGCCTGT GGGAACCAAGGAGGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	TACACACTTCTTACCCATTCACTGAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACTCCAGCTTCTCAGCTCTGCTGCTGCTGCTGCTGCA AGGGTTTGTCTTAATCTCAATCAATGTCTCTTCATCTTTAGCAGCTGTGGGTTTTGTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTTAATTATAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAAGTTCACAACATTTATTAATAAAATTTTTCACCTG
ESTD-MCC	--	--	--	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCAGCTCTGCTCCTAGCCGAACITCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGGATCCCCGAA TCTCAGGAAGTCTGCTCTTCCAAAGGGTTGGTCTAAGTTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGTTCTGTTTGTAGCATGG
ESTD-NF1	--	--	--	---	---	ATTATCCAGATGAATTTACAAAACATATACCAGATCCCACAGACTGATATGGCTGGT

ESTD- NFKB1	--	--	--	---	---	AACATGGACTTGATATTTGTACAAAAAAGTTTTATTTTCTAAAAAAGAAAAAAGAAAA AAATTTAAGGGTGACTTATATCCACACTGCACACTGCCTAGCCCAAAACGCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGTTGCTTTGTGAACCTTTGTAGGGGACGAGAAAGATCATTTGAAATTTCTGAG AAACCTCTTTTAAACCTCACCTTTGTGGGGTTTTGGAGAAGGTTATCA
ESTD- NPPA	--	--	--	---	---	TGTCCCTAGGCCCCAGCCCTGCTTGTCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAGAACACAGAC AT
ESTD- NRAMP	--	--	--	---	---	GGAGGAGGAGGTGGGGAGGGGGTCTGTCTGCTCCAGGTOCCACAGACAGAGAGGCGGCCCTCAGTG TATCCCCACCCCAATGTGGGGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD- NRAS	--	--	--	---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGTTTTCTTTATGTAGGGTGATATGGATACCTTTTGTGTGATTATATAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTTGC ATTCCCTGTGGTTTTTAATAAAAT
ESTD-OTC	--	--	--	---	---	GTGACCTTCTCACCTTTAAAAACCTTACCGGAGAAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
ESTD-PAI1	--	--	--	---	---	GCCACCACCCACCACACACCTCCAACTCAGCCAGACAGGTTGTTGACACAAGAGAGCCCC TCAGGGCACAGAGAGAGTCTGGACACGTGGGGAGTCAGCGTGTATCATCGAGGGCGCGGCAC ATGGCAGGGATGAGGGAAAGACCAAGAGTCTCTGTTGGGCCAAGTCTCTAGACAGACAAAAACCTAG ACAATCAGGTGGCTGGCT
ESTD-PAR	--	--	--	---	---	CTCTTCAGGAACACAGTCTCTTACCAACACAGCACTTATTGCTGTCGAGAGGTACAACCCGTAGA ACTTCTTCTAAGTAACTTATAGTTAAGGAATCGAAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTTCAATAGCTGTGAGTGTCTTCTTCTTCTTCTGTTCTAGAACGTTTCTTAG GACTGGCAGTTTAAAGCTTTCACCTAGGCTTCTGTATACCCATGCC
ESTD- PBD4	--	--	--	---	---	CCTTCTCATGCCAGATGGAATTCAGTCCCTTCAAGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGCACTAATCCAAATCTCTACCCGAGCTTGCCTGCATACAGCG GACAGTGTGGTGGCAACATTGAAGCCTCGTACC
ESTD-PS-1	--	--	--	---	---	GGGAGTAAACCTGGATTGGGAGATTTCATTTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCATAGCCTATTCTGAGCCATATAATTTGTTGTGCCCTACATT ATTACTCTTGGCAATTTCAAGAAAGCATTGCAGCTCTTCCAAATCTCCATCACCTTTGGGCTTGT CTACTTTGCCACAGATTATCTTGTA
ESTD- PXMP1	--	--	--	---	---	ATGAAACATGGTCTTTAAATTTATGATATGTTGTTATAGCTATTTAAAGGGCTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGTGACAAAGTGTTTTCTCAAGGCTCATACAGA TTCTGAAATCATGGTCCCTAGAACATTTTGAAGAGGTAAGTCTTATGAAATTAATCTT
ESTD- Per/RDS	--	--	--	---	---	ACCTACAGACGTGCTGGATGGTGTGTCTCCAAACCCGAGGAATCTGAGAGCGAGAGAGGGCTGGCTG CTGGAGAAGAGCGTGGCGGAGACCTGGAAAGGCT



ESTD-FDS	--	--	--	---	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGCTGGAGAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGAAGAAGCTGGCAAGGGCAACAGGTGGAAGCCGAGGGCGCAGACGCAGG CCAGCCCCAGAGCGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCAACACTGAGAAATAGTGCAC CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	---	---	---	CTTCGTGACGGAGGTACGCTCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCC CTGTGACAGTATGACAGCGACACTTGTCTACTATGAGAGGGGAGCTGTGTGACATCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGATCAGCTGAGTGGAGGCCACCTGCCCTGGGGCCAGCCACT CCGAGTCGGCATGTCACTACCGGGCAGTACCTAGCGCTACCGAGG
ESTD- SPTB	--	--	---	---	---	TGAACACCCCTGTGTCGGAGCCAGGTGTGTTCTCCTGGGAGCCTGAGGAGTTTGTGTGTGTG CAGTCCCCCGGCCACTGCTGTTGAGCCTGGACATACACCTTCACCTCCTTTGGCCCGGAGAGAC ATTTACCCACTGGCCATGTCCTGGCTGTTGTGCACACCCCTCTGTGAAGACCCCAACCCCTGCCTCC CCACCCCAAGCCAGTTTCCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	---	---	---	TTCACTTTGTGGATTGTTCTTTTGTGTGCAGCACCTTTCAACATGATGTATCCCATTTGTCCAAG TTTGTCTTGGCTGCCCTGTGCTGTGGGATATTTGAAGAGATCTTTGCCAGTCCAATGTCTAGAGAG TTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTAAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	--	--	---	---	---	AAATGGTCAGGACCCTGATCCACAAGAAAGTGTGACCATTTTCATCAGGGCCATCAGTTTCATCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCAATCATCTTAAATGACTTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACTTTCTCCAGTATGGATGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACACATCA
ESTD- THR8	--	--	---	---	---	TGCGGCTTTCTCCGGCAGGGTAGACTCTTACTTGGCTGTGATTTCCAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	---	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCAGACCTGGTCCCCAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTTCCAGCTCCAGGCTCTACACACAAATCAGTCAGTG GCCAGAAGACCCCCCTCAGATCGGAGCAGGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCTCCCACTTTCCAAATCCCGCCCGCGATGG
ESTD-TYR	--	--	---	---	---	TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGATTCTTGTTCACCCGCAACAAGAGTCTATGC CAAGCGAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATATGCATCCAGACAAAGAGGTCAATAATTTGATGTGCTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCTATGGGGATGACA

ESTD- TYRP1	--	--	---	---	---	AGTAGTGATGAAGCTAACGAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCAATAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATACTGTATTTCTTTCACTTTATTACCTTCTTCT AATACAAGCATATGTTAGAATTAAAGTTCTAGGCATACCTT
ESTD- VB12	--	--	---	---	---	TTCCCAAGGCTCAATACAAGCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTCACAGAGACAGGAACACCAAGTG ACTTGAGATGTCACCAAGACTGAGAACCCAGTTATATGTACTGTATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	---	---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTCTTGG TCCCTAGAGTCTG
ESTD-WT1	--	--	---	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CGACGTGTGCTGGAGTAGCCCGGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAAGGCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD- s14544	--	--	---	---	---	TTGGGAAGTTAGAGCCTATATAAATTACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAA TATCCCAAAGTTGAAATGCTCAGTTCGCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTAACC TCT
EST71770 6	--	--	---	---	---	AGCACCACTCTCAGTCAAGCCTCAGCACCAAGATGCTGTTCTATAAGGATGACGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAACCACCTGCAGAGTACCAGCTGTTGGTGAAGG AGTGCCCACTCCAGGCTGACACTGGACAAGAAAGAGGCCATCCAAGG
EST52418 6	--	--	---	---	---	CAAAATTACAGGGTCAACTGCTATGATGTGTTGGAGCCCAAGTCACCCCTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAAACTGTGAGTGTGG
EST13586 3	--	--	---	---	---	CCCACCTCTATTGCCCCAGCCCCAGGACAGAGCTGATCCTTGAACCTTAAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCAGCCCCAGACCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCCTGCCCGG GTCACTC
EST51976 7	--	--	---	---	---	AGGCAGAACTGGGCCCCCATCGGGGGGACGTGGGAAGGCCACTTGAGCTTCCTGGAGAAGGACCTGA GGGACAAAGGTCAACTCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACACAGCAGCAGGAGCAGCAGGAGGAGGTGCAGATGCTGGCC CCTTGGAGAGCTGAGCTGCCCCCTGGTGC

-301-

EST11458 6	--	--	---	---	---	CCACCTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCAAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAATAAACATTCTATGAGCCAGGAGAGATACGTAATTCCTGCAAGCCGGCTATGTGTC CGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	---	---	---	CGGTCTCCTCCAGGTATTGTTGCAGAAGCCGAGATGACCTCTATGTCAGATGCATTCCATAAG GCATTTCTGAGGTGAGTACACCTTCCCCACTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACAGTGGAAAGGCCTGTTCCAGTGTTAAGGCATGCAAAAGCCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	---	---	---	ACCTGGTGTGCTGGTGTGGGTGAACCTGGTCTCTTGCCATTGCCGGCCCTCTCTGGGGCCCGTGG TCCTCTGGTGTGCTGGGTAGTCTGGAGTCAACGGTGTCTCTAGTGAAGCTGGTGTGATGGCAACC CTGGGAACGATGTTCCCTCCAGGTGCGGATGTTCAACCCGACACAAGGAGAGCGCGGTTACCCCTGG CAATAT
EST36027 2	--	--	---	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCTGCTGGCCAACTATGCTCTCAGA ACATCACTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCACTTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTTGTAGTGGTGTCTAAAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	---	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAAATAGAGCCCTACCAAGTGTAT TACATAAAGAAAGTCAAGTGTTTACTCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTGA TAGTAAATGACCGATGGGTGAGAACTGTTCTGTCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 EST44438 7	--	--	---	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGTCTCTCCAGGGCCCTGTCTATC CAGTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCAACACTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCAGCCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	--	--	---	---	---	TGCAAAACACACAAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTGTCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGAAACTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
EST54419 8	--	--	---	---	---	CTTCTGCCTAATTGAATGATATTGTTGCTGTGGGACCTGAGCACCTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTGTATGTTGCTACTA TAGTCCAAAGTGAA

EST10398 2	--	--	--	---	---	TGCTGGGTGGCAAGGCTGCAACAAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTTACATTTGGGGCTTGACTTTCCACACGGAAG CATTGTTTCTCGGGCAAGAAGGTATCTACCAATAGTGTCATTAGGCAITTG
EST36751 7	--	--	--	---	---	CCAGTGTTCAATTTAGCTTGCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAATATGAACCTTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	--	--	--	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGATCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCAATTATAACAAATATTTTACCTTTTGAAAAAATAATG AAGGATTGACCTGCTTCGCTCTGAAAGAGTATCCGTACCGTCTGACGTTTGAAACAATACAGAT GCCTTCCCTGTAGCAGTTTCAGCCTCCTCTACCCCTA
EST18288 3	--	--	--	---	---	GCTCTATACCCCTGTGCTCCACGCTCTCTGGACTTCACAGAACTGGATTTGCTGCTGAGAA GATTACAGGTTTCATGACGGCTGTACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTCAACACCTAGTCCACTTCCAAGGTAAAGCAACCTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	--	---	---	TTCCGCCAGCCCCCATCTTGGCACCCCTGGTCCCCCTAGGGGCCAOCOCGGGCACTCACCGCTCT CGCTCTCGGTAAACATCCGGCCGGCGCCGCTCTTGAGCACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCCCTGTCCGGGCTTGCACGGGGCAGCCCTGCAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACAGTG
EST58707 7	--	--	--	---	---	CAGTGATCTGGAAGCCTACAGGACACCAAAATACCTTAATCATCAATTTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATCCGAGAGACCCCTAGAAGATACACGAGACCGA ATGATCAATGGACATTCAGCAGGAACITCAAGATACCTGTCTCTGGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCCTT
EST74167 6	--	--	--	---	---	AGACCATGAAGGAGTTGAAGGCTTACAAATCGGAATCGGAATCGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGGGCGGCGAGCCCGGCTGGGCGGAGCATGGAGGA CGTCGCGGCGCGCTGGTGCAGTACCGCGCGAGGTGCAAGCCATGCTCGGCCAGAGCACCCGAGGAGC TGCGGCTGCGCTCGCTCCACCTCGCAAGCTGCGTAAGCGGCTCCTC
EST43211 8	--	--	--	---	---	CGCTGTGTCAGTAOCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCAGAACGCGCC TGGCAGTGTACAGGCGGCGGCGGAGGGCGCGAGCGGCGCTCAGCGCCATCCGCGAGCGCGCTG GGGCGCTGTGTGAACAGGGCGCGGTGCGGGCGCGCCACTGTGGGCTC
EST36770 4	--	--	--	---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGCCAGTTGCCAGCTATAATCC ATCGAAATGATTTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAAATATACTGGGTTTCTGTTTCTTTCTGATCAT TCTTACAAGTTATACTCTTATTGGAAGGCCCTAAAGAAGGCTTATG

EST26021 1	--	--	--	---	---	TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTTGAGGTTGAGTGACATGTTCCGAAACCTGT CCATAAAGTAATTTGTGAAAGAGGAGCAAGAGAACTTCTCTGCAGCACTTCACTACCAAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTCTTCTTTGCAACAAGACAAAAGGCC
EST51212 0	--	--	--	---	---	ATCCTGAGCTCGCAATAAGCTTCTTGGTTCTACTTCTCTCCACAAGCCCAATTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCCTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	--	---	---	GTTCGAAATCCTCCTCTGAAAGTGGCCGGTTTAACTGCTCATGACGCTGCGGCTGIGGTCAGCT GAGGTGAGGGGCTTGAAGCTGGGAGTGGGTTTAGGACGCGGCTCTCTGCTGCATCCTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGCTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	--	---	---	ACAATCAGGTCACACATTCCAGAAGAGGAGGGTGGTCAAGTGGCTGGGTAGGTCAGTAATCCA AGGATTCAGGAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	--	---	---	CTTCTATGGGATTGACTTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGAGCTCATGACAATTTGAAGCTGACAATACACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACCTTGGTGTACCTTTAATTACAACCTAG CAGACGGAAGTGAAGTCAAGGTAAGAAT
EST34088 2	--	--	--	---	---	GTGGGGCAACAGTGGGAGAGAGGGGGCCAGGGTATAAAGGGGGCCACAAGAGACCGGCTCAAGG ATCCCAAGGGCCCAACTCCCGAACCACTCAGGGTCTCTGTGGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTTCCCTTGGGA CTTTGAGTCAAAATTGGCTGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAGGACCCCAAGAAAT CACAGGTGGCAAGTGGCTTACCGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082	--	--	--	---	---	TCAGGGTGGCTGGACCCAGGCCCAAGCTCTGCAGCAGGAGGACGTTGGCTGGGCTGCTGAAGCATG TGGGGTGAGCCAGGGGGCCCAAGGCAGGGCACTGGCTTTCAGCTGCTCAGCCCTGCTGCTGCTC CCAGTCACTGCTCTTCTGCCATGGCCCTGTGGATGGCTCTCTGCCCTGCTGGCGCTGCTGGCCCTC TGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGGG
EST45311 0	--	--	--	---	---	GGCCTCTCTCTTCCAAATCTGTCCCTATAGTTTCCCTCTATTAAAGTGAACATGCAATCTTTTAGT GGATAGATGCACACAAACACACAAGCCATTATGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTTCATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTGTGAAT

EST65258 8							TGCCCCATCAGCGCGGAGACATGGCTTGCCACAGCTCTTGAGATGTCACCAATTAACCCAGAAAT CCAGTTATTTCCACCTCAAAATGACAGCCATGCCGCGGGTCTTCTGGGGCTCGTCGGGGG ACAGCTCCACTCTGACTGGCAGCTTTTGATGGAGACTTGAGGAGGAGGGCTTGAGGTTGGTGAG GTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3							ATGAGGATGAAGGTGGACAGGAGGAGAGGGCCAACTGTGATCCCGGGCTGCAGATGTGCTG GACTATGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782							ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTAATAGCATTTGTTTAGCATTAACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTTACCTTAATGCTTATTTTAAATGACAGTGGAAG TTTTTTTTCCTCGAAGTCCAGTATCCAGAGTTTGGTTTTTGAAC TAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGTCTTGGGGTTTTTGTGTCATGCA
EST35879 9							GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGCGGTTCCACCGATG GAACTGCCGGCAATCCTGACACGTGTGCACCGGCTGTACCCAAATAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCGAAGACAGCAGCGGATGGGGCAGGAGAGAGCTGCCTGGATGAA
EST68308 5							GGAAAGAGATTAAAGAGCTTGATTTGGACAATCTGGTTCTTTGAGTGTGGAAGAGTTTCATGTCTCT GCCTGAGTTACACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGTAAGAAAGTAGTTATTTTTTA
EST54045 6							GGAAATTTAAAAATATTTAAATACCTCCATTTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAATCT GTTAAGTAAGTACTGTTTGGCCTTGGAAATGGATTTTAAATGTGACTTTATCAT
EST52908 0							ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTTGGGAGAGATGGATGGTGTGCAAGCCCTTTGG CAATGTGAGATTGTATG
EST19590							AGGAGAAGCTGAGGAGGGGAAGAGAGACAAAGATGACATTGATGAGTGAAGATGTGCGGCTCAGGAT GCCGGAATGAC
EST76136							TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACCCCGGTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT
EST58607 0							CTCTGGATGGGTTACAGGTGGCAGGCACAAAGCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCCTACATGGAGAACAGGACAGCACATGGCGGGATGGCGCGGGAGTTCTGGT TGCGGCCACGGCTGTGGCTCTGTTGTGAACGGTAGCCTTTGGGTTGCGATGCCTAAACCTTTGTTCT TGCCCAAGGAGGGCGGGTGCCATGCCTGAGATGTAGATGCGGGC
							Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

-305-

## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

-306-

## CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a  
20 segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.



-307-

12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which  
10 is selected from the group consisting of the nucleotide  
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining  
comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.

-308-

20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
- 5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.